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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:49:03 ; Search time 28.2625 Seconds
(without alignments)
279.234 Million cell updates/sec

Title: US-10-049-868A-3
Perfect score: 606
Sequence: 1 DIETQSPAINMSASGPEKVT.....GTKLELKRADAAPTIVSIFKL 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	75.6	235	3	US-09-171-945-17
2	445	73.4	215	6	5455030-3
3	445	73.4	235	2	US-08-303-569B-5
4	445	73.4	235	2	US-08-116-247-5
5	445	73.4	235	4	US-09-795-515-5
6	445	73.4	235	4	US-09-348-224-5
7	444	73.3	255	3	US-09-553-498-8
8	444	73.3	255	4	US-09-618-869-8
9	443.5	73.2	213	2	US-08-737-129A-4
10	439	72.4	108	3	US-09-171-945-9
11	427	70.5	256	4	US-09-526-738A-2
12	427	70.5	258	4	US-09-526-738A-4
13	426	70.3	270	2	US-08-652-507-2
14	426	70.3	553	3	US-08-661-052-16
15	426	70.3	553	3	US-09-188-082-16
16	426	70.3	553	3	US-09-364-088-16
17	426	70.3	553	3	US-09-102-716-16
18	425	70.1	223	3	US-08-190-199A-63
19	425	70.1	235	4	US-09-423-439-58
20	425	70.1	235	3	US-09-011-769A-23
21	425	70.1	236	2	US-08-190-199A-65
22	424	70.0	222	2	US-08-190-199A-67
23	424	70.0	235	2	US-08-190-199A-61
24	420	69.3	106	2	US-08-956-047-33
25	420	69.3	128	2	US-08-956-047-31
26	420	69.3	240	2	US-08-956-047-25
27	420	69.3	281	3	US-09-423-439-44

28	420	69.3	666	3	US-09-423-439-51	Sequence 51, Appl
29	417	68.8	108	4	US-09-948-004-28	Sequence 28, Appl
30	417	68.8	495	4	US-09-948-004-18	Sequence 18, Appl
31	414	68.3	103	1	US-08-467-393-4	Sequence 4, Appl
32	414	68.3	144	4	US-09-318-786-29	Sequence 29, Appl
33	413	68.2	129	2	US-08-116-778B-2	Sequence 2, Appl
34	413	68.2	129	2	US-08-438-562-2	Sequence 92, Appl
35	413	68.2	129	2	US-08-483-528B-92	Sequence 2, Appl
36	413	68.2	242	2	US-08-553-497A-28	Sequence 28, Appl
37	410.5	67.7	107	1	US-07-942-245-3	Sequence 3, Appl
38	409.5	67.6	110	3	US-08-836-561-33	Sequence 33, Appl
39	409.5	67.6	110	4	US-09-434-122-33	Sequence 33, Appl
40	409	67.5	106	3	US-08-397-411-9	Sequence 9, Appl
41	408	67.3	599	1	US-08-463-163-3	Sequence 3, Appl
42	408	67.3	100	2	US-08-308-494A-19	Sequence 19, Appl
43	408	67.3	106	1	US-07-634-278-1	Sequence 1, Appl
44	408	67.3	106	1	US-07-634-278-16	Sequence 16, Appl
45	408	67.3	106	1	US-08-477-728-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-171-945-17
; Sequence 17, Application US/09171945
; Patent No. 6277599

; GENERAL INFORMATION:

; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham

; APPLICANT: Edge, Michael Derek

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System

; FILE REFERENCE: Monoclonal Antibody to CEA

; CURRENT APPLICATION NUMBER: US/09/171,945

; PRIOR FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: GB9703103.3

; PRIOR FILING DATE: 1997-02-14

; PRIOR APPLICATION NUMBER: GB9609405.7

; PRIOR FILING DATE: 1996-05-04

; PRIOR APPLICATION NUMBER: PCT/GB97/01165

; PRIOR FILING DATE: 1997-04-29

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-17

Query Match 75.6%; Score 458; DB 3; Length 235;

Best Local Similarity 76.9%; Pred. No. 1.2e-41;

Matches 90; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIETQSPAINMSASGPEKVTTCSSASSVYMHWFQESGTPPKRIYDTSKLSGVDPAR 60

DB 23 DIETQSPAINMSASGPEKVTTCSSASSVYMHWFQESGTPPKRIYDTSKLSGVDPAR 82

QY 61 LSGSGSGTFTLEISRKAEDGVVYCCQLVEYPLTFGAGTKLELKRADAAPTIVSIF 117

DB 83 FSGSGSGTFTLEISRKAEDGVVYCCQLVEYPLTFGAGTKLELKRADAAPTIVSIF 139

RESULT 2

5455030-3

; Patent No. 5455030

; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL

; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN

; POLYPEPTIDE BINDING MOLECULES

; NUMBER OF SEQUENCES: 24

; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/40,440
/ FILING DATE: 1-APR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 512,910
/ FILING DATE: 25-APR-1990
/ APPLICATION NUMBER: 299,617
/ FILING DATE: 19-JAN-1989
/ APPLICATION NUMBER: 92,110
/ FILING DATE: 02-SEP-1987
/ APPLICATION NUMBER: 902,971
/ FILING DATE: 01-SEP-1986
/ SEQ ID NO:3:
/ LENGTH: 215
5455030-3

Query Match 73.4%; Score 445; DB 6; Length 215;
Best Local Similarity 77.6%; Pred. No. 2.8e-40;
Matches 90; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 4 LTQSPAIMSASPGKVTMTCSASSV--NYMHWFQESGTFPKRIYDTSKLASGVPARL 61
Db 4 LTQSPAIMSASPGKVTMTCSASSVSSYLHWFOQKSGASPKLWIYSTNLASGVPARF 63
QY 62 SGSGSGTEFTLEISRVAEDGVVYCCQLVVEYPLTFGAGTKLEKRAADAAPTYSIF 117
Db 64 SGSGSGTSYSLTISGMEADAATYCCQWSSNPFTEGSGTKLEINRADTAPTYSIF 119

RESULT 3
US-08-303-569B-5
; Sequence 5, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Irujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-303-569B-5

Query Match 73.4%; Score 445; DB 2; Length 235;
Best Local Similarity 75.0%; Pred. No. 3.1e-40;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNYMHWFQESGTFPKRIYDTSKLASGVPARL 61
Db 24 IVLTQSPAIMSASPGKVTMTCSASSVSNMNYQKSGTSPKRWIYDTSKLASGVPAHF 83
QY 62 SGSGSGTEFTLEISRVAEDGVVYCCQLVVEYPLTFGAGTKLEKRAADAAPTYSIF 117
Db 84 RSGSGSGTSYSLTISGMEADAATYCCQWSSNPFTEGSGTKLEINRADTAPTYSIF 139

RESULT 4
US-08-116-247-5
; Sequence 5, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-247-5

Query Match 73.4%; Score 445; DB 2; Length 235;
Best Local Similarity 75.0%; Pred. No. 3.1e-40;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNYMHWFQESGTFPKRIYDTSKLASGVPARL 61
Db 24 IVLTQSPAIMSASPGKVTMTCSASSVSNMNYQKSGTSPKRWIYDTSKLASGVPAHF 83
QY 62 SGSGSGTEFTLEISRVAEDGVVYCCQLVVEYPLTFGAGTKLEKRAADAAPTYSIF 117
Db 84 RSGSGSGTSYSLTISGMEADAATYCCQWSSNPFTEGSGTKLEINRADTAPTYSIF 139

RESULT 5
US-09-795-515-5
; Sequence 5, Application US/09795515
; Patent No. 6632927
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
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; ORGANISM: Mouse
US-09-348-224-5

Query Match 73.4%; Score 445; DB 4; Length 235;
Best Local Similarity 75.0%; Pred. No. 3.1e-40;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSAPGKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLAGVDPARL 61
DB 24 IVLTQSPAIMSAPGKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLAGVDPARL 83

QY 62 SGSGSGTEFTLEISRKAEDVGYYVYQQLVEYPLTFGAGTKLELKRADAAPTYSIF 117
DB 84 RGS GSGTSYLTISGMEADAAYYCQWSSNFTFGSGTKLEINRADTAPTYSIF 139

RESULT 7
US-09-553-498-8
; Sequence 8, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted proteins
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-8

Query Match 73.3%; Score 444; DB 3; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-40;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSAPGKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLAGVDPAR 60
DB 132 DIELTQSPAIMSAPGKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLAGVDPAR 191

QY 61 LSGSGSGTEFTLEISRKAEDVGYYVYQQLVEYPLTFGAGTKLELKRADA 110
DB 192 FSGSGSGTSYLTISGMEADAAYYCQWSSNPLTFGAGTKLELKRAAA 241

RESULT 8
US-09-618-869-8
; Sequence 8, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR CHAPERONES
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT

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; ORGANISM: Escherichia coli
US-09-618-869-8

Query Match 73.3%; Score 444; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-40;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 60
Db 132 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 191
QY 61 LSGSGSGTFTLEISRVAEDGVVYCCQQLVEYPLTFGAGTKLELKRADA 110
Db 192 FSGSGSGTSYSLTISRMEADAATYCCQWSSNPLTFGAGTKLELKRADA 241

RESULT 9

US-08-737-129A-4
; Sequence 4, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLISING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:

TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-4

Query Match 73.2%; Score 443.5; DB 2; Length 213;
Best Local Similarity 73.5%; Pred. No. 4e-40;
Matches 86; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 60
Db 1 ELVMTQTFAIMSASPGKVTMTCSASSISYHHVYQQKPGTFPKRIYDTSKLAGVGP 60
QY 61 LSGSGSGTFTLEISRVAEDGVVYCCQQLVEYPLTFGAGTKLELKRADAAPTYSIF 117
Db 61 FSGSGSGTSYSLTISRMEADAATYCHQRSYP-TFGGTYKLEIKRADAAPTYSIF 116

RESULT 10

US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patencin ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match 72.4%; Score 439; DB 3; Length 108;
Best Local Similarity 79.6%; Pred. No. 5.1e-40;
Matches 86; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 60
Db 1 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 60
QY 61 LSGSGSGTFTLEISRVAEDGVVYCCQQLVEYPLTFGAGTKLELKRADA 108
Db 61 FSGSGSGTSYSLTISRMEADAATYCCQORSTYPLTFGAGTKLELKRADA 108

RESULT 11

US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-2

Query Match 70.5%; Score 427; DB 4; Length 256;
Best Local Similarity 73.7%; Pred. No. 3e-38;
Matches 84; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 60
Db 132 DIETQSPAIMSASPGKVTMTCSASSVNMVHWFQESGTFPKRIYDTSKLAGVGP 191
QY 61 LSGSGSGTFTLEISRVAEDGVVYCCQQLVEYPLTFGAGTKLELKRADAAPT 114
Db 192 FSGSGSGTSYSLTISRMEADAATYCCQORSSYPYTFGGTKLQIKRAAGAPV 245

Wed Oct 13 13:59:33 2004

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RESULT 12
US-09-526-738A-4
; Sequence 4, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526, 738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-4

Query Match      70.5%; Score 427; DB 4; Length 258;
Best Local Similarity 73.7%; Pred. No. 3.1e-38;
Matches 84; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPAR 60
Db 134 DIETQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPAR 193
QY 61 LSGSGSTFTLEISRVAEDVGVYCCQOLVVEYPLTFGAGTKLEKRAADAPT 114
Db 194 FSGSGSTFTLEISRVAEDVGVYCCQOLVVEYPLTFGAGTKLEKRAADAPT 247

RESULT 13
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5976691
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-507-2

Query Match      70.5%; Score 427; DB 4; Length 258;
Best Local Similarity 73.7%; Pred. No. 3.1e-38;
Matches 84; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPAR 60
Db 134 DIETQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPAR 193
QY 61 LSGSGSTFTLEISRVAEDVGVYCCQOLVVEYPLTFGAGTKLEKRAADAPT 114
Db 194 FSGSGSTFTLEISRVAEDVGVYCCQOLVVEYPLTFGAGTKLEKRAADAPT 247

RESULT 14
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezhian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-16

Query Match      70.3%; Score 426; DB 2; Length 553;
Best Local Similarity 79.0%; Pred. No. 1e-37;
Matches 83; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARLSG 63
Db 165 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARLSG 224
QY 64 SSGSGTEFTLEISRVAEDVGVYCCQOLVVEYPLTFGAGTKLEKRA 108
Db 225 SSGSGTSYSLTISRMEADAATYTCQORSSYPITFGAGTKLEKRA 269

RESULT 15
US-08-652-507-2

Query Match      70.3%; Score 426; DB 2; Length 553;
Best Local Similarity 79.0%; Pred. No. 1e-37;
Matches 83; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARLSG 63
Db 165 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARLSG 224
QY 64 SSGSGTEFTLEISRVAEDVGVYCCQOLVVEYPLTFGAGTKLEKRA 108
Db 225 SSGSGTSYSLTISRMEADAATYTCQORSSYPITFGAGTKLEKRA 269
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Query Match	70.3%	Score 426;	DB 3;	Length 553;
Best Local Similarity	79.0%;	Pred. No. 1e-37;		
Matches	83;	Conservative	7;	Mismatches 15; Indels 0; Gaps 0;

QY	4	LTQSPALMSASPGEKV	MTCTCSASSSYNMHW	FQESGTFPKRR	YDTSKIASGVP	PARLSG	63
Db	415	LTQSPALMSASPGEKV	ITCTCSASSSYNMHW	FQKPGTSPKLI	WTSTNLS	ASGVP	474
QY	64	SSGSSEFTTLEISRVKAE	DGVVYCCQQLV	YPLTF	FGAGTKLEL	KRA	108
Db	475	SSGSYTSYLTIRMEAE	DAATYTCQQRSS	YPITFGAGTKLEL	KRA	519	

Search completed: October 13, 2004, 13:01:09
Job time : 30.2625 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:12:35 ; Search time 21.8705 Seconds
(without alignments)
2201.453 Million cell updates/sec

Title: US-10-049-868A-2

Perfect score: 673
Sequence: 1 caggtgcagctcaggagtc.....ccaggtcaccgtctctctca 363

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Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538	79.9	222	US-08-190-189A-67	Sequence 67, Appl
2	538	79.9	235	US-08-190-155A-61	Sequence 61, Appl
3	535.5	79.6	120	US-08-652-558-38	Sequence 38, Appl
4	535	79.5	119	US-08-752-844-16	Sequence 16, Appl
5	535	79.5	119	US-08-591-196-16	Sequence 16, Appl
6	535	79.5	119	US-09-293-533-16	Sequence 16, Appl
7	531.5	79.0	140	US-08-943-136-4	Sequence 4, Appl
8	531.5	79.0	140	US-08-973-518-4	Sequence 4, Appl
9	529.5	78.7	242	US-08-973-518-4	Patent No. 5455030
10	525.5	78.1	121	US-08-881-037-67	Sequence 67, Appl
11	523	77.7	119	US-08-667-769A-15	Sequence 15, Appl
12	523	77.7	119	PCT-US95-17082A-15	Sequence 15, Appl

13	521.5	77.5	112	3	US-09-189-129-3	Sequence 3, Appl
14	521.5	77.5	112	4	US-09-824-286-3	Sequence 3, Appl
15	517.5	76.9	239	2	US-08-860-174A-2	Sequence 2, Appl
16	515	76.5	119	3	US-08-483-749A-14	Sequence 14, Appl
17	512.5	76.2	137	2	US-08-621-751A-4	Sequence 4, Appl
18	507.5	75.4	239	6	5455030-13	Patent No. 5455030
19	505.5	75.1	241	4	US-09-554-765-13	Sequence 13, Appl
20	499.5	74.2	116	3	US-08-397-411-4	Sequence 4, Appl
21	498.5	74.1	272	4	US-08-756-416-39	Sequence 39, Appl
22	498	74.0	113	2	US-08-606-293-2	Sequence 2, Appl
23	489	72.7	111	1	US-08-467-420A-15	Sequence 15, Appl
24	489	72.7	111	1	US-08-470-110A-15	Sequence 15, Appl
25	489	72.7	111	2	US-08-940-371-15	Sequence 15, Appl
26	489	72.7	111	3	US-08-637-647-15	Sequence 15, Appl
27	488	72.5	115	3	US-08-881-037-22	Sequence 22, Appl
28	484	71.9	97	3	US-08-881-037-66	Sequence 66, Appl
29	478	71.0	113	2	US-08-606-293-6	Sequence 6, Appl
30	476	70.7	152	2	US-08-752-844-4	Sequence 4, Appl
31	476	70.7	152	2	US-08-591-196-4	Sequence 4, Appl
32	476	70.7	152	3	US-09-192-838B-4	Sequence 4, Appl
33	476	70.7	152	4	US-09-293-533-4	Sequence 4, Appl
34	476	70.7	152	4	US-09-324-191-4	Sequence 4, Appl
35	476	70.7	263	2	US-08-752-844-66	Sequence 66, Appl
36	476	70.7	263	4	US-09-293-533-66	Sequence 8, Appl
37	473.5	70.4	120	2	US-08-652-558-8	Sequence 8, Appl
38	473.5	70.4	120	3	US-09-254-189-5	Sequence 5, Appl
39	473	70.3	107	1	US-08-122-546-12	Sequence 12, Appl
40	473	70.3	107	2	US-08-764-938-12	Sequence 12, Appl
41	473	70.3	107	3	US-09-131-052-12	Sequence 12, Appl
42	473	70.3	107	3	US-09-131-053A-12	Sequence 12, Appl
43	472	70.1	264	3	US-08-564-164A-4	Sequence 4, Appl
44	471.5	70.1	107	1	US-07-942-245-14	Sequence 14, Appl
45	469.5	69.8	215	4	US-09-170-769A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-08-190-199A-67
; Sequence 67, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHEV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: PCT/GB92/01483
; APPLICATION NUMBER: 10-AUG-1992
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991

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/ INFORMATION FOR SEQ ID NO: 67:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 222 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-190-199A-67

Alignment Scores:
Pred. No.: 1 62e-59 Length: 222
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-190-199A-67 (1-222)
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Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTCACATCTCTCGGGATTTCATTAACACAGATATGGTGACACTGGGTTCCGCGCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTCGAGTGGCTGGGAGTAATATGAGCTGGTGAAGCAACAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGACAACCTCCAGAGCCAACTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAATGAACAGCTGCAGACTGATCAGACAGCATGATGAGTGGTGGAGCAACAATATAAT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCTATGCTATGAGTACTGGGCGCCAGGACCAAGGACCAAGTCTCC 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113

RESULT 2
US-08-190-199A-61
/ Sequence 61, Application US/08190199A
/ Patent No. 5830663
/ GENERAL INFORMATION:
/ APPLICANT: EMBLETON, Michael J.
/ APPLICANT: GOROCIOV, Guy
/ APPLICANT: JONES, Peter T.
/ APPLICANT: WINTER, Gregory P.
/ TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/190,199A
/ FILING DATE: 13-JUL-1994
/ CLASSIFICATION: 435

PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB92/01483
/ FILING DATE: 10-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9212419.7
/ FILING DATE: 11-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9117352.6
/ FILING DATE: 10-AUG-1991
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 235 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-190-199A-61

Alignment Scores:
Pred. No.: 1 66e-59 Length: 235
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-190-199A-61 (1-235)
QY 1 CAGGTGCAGCTGCAGAGTCTGGAGCTGGCGCTGGCGCCCTCAGAGCGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTCACATCTCTCGGGATTTCATTAACACAGATATGGTGACACTGGGTTCCGCGCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTCGAGTGGCTGGGAGTAATATGAGTGGTGAAGCAACAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGACAACCTCCAGAGCCAACTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAATGAACAGCTGCAGACTGATCAGACAGCATGATGAGTGGTGGAGCAACAATATAAT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCTATGCTATGAGTACTGGGCGCCAGGACCAAGGACCAAGTCTCC 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113

RESULT 3
US-08-652-558-38
/ Sequence 38, Application US/08652558
/ Patent No. 5861155
/ GENERAL INFORMATION:
/ APPLICANT: LIN, AUGUSTINE YEE-THARN
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
/ THEREOF
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BANNER & WITCOFF
/ STREET: 75 STATE STREET, 23RD FLOOR
/ CITY: BOSTON
/ STATE: MASSACHUSETTS
/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
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; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wordperfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/652,558
 ; FILING DATE: JUNE 6, 1996
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/IB94/00387
 ; FILING DATE: NOVEMBER 21, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: YANKWICH, LEON R.
 ; REGISTRATION NUMBER: 30,237
 ; REFERENCE/DOCKET NUMBER: 95,497-L
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-9100
 ; TELEFAX: 617-345-9111
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-652-558-38

Alignment Scores:
 Pred. No.: 2,6e-59 Length: 120
 Score: 535.50 Matches: 104
 Percent Similarity: 90.91% Conservative: 6
 Best Local Similarity: 85.95% Mismatches: 10
 Query Match: 79.57% Indels: 1
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-652-558-38 (1-120)

QY 1 CAGTGCAGCTCGAGAGTCTGGAGCTGGCTGGCTGGCGCCCTCACAGAGCTGTCCATC 60
 DB 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
 QY 61 ACTTGCACTGTCTGGGATTTCAATAACAGATATGTGTACACTGGGTTCGCCAGCCT 120
 DB 21 ThrCysThrValSerGlyPheSerLeuThrAlaTyrGlyValAsnTrpValArgGlnPro 40
 QY 121 CCAGAAAGGCTCTGGAGTCTGGAGTAATATGAGTCTGGTGGGAGCACAATAATTAAT 180
 DB 41 ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlyAsnThrAspTyrAsn 60
 QY 181 TCGGCTCTCATGTCAGACTCAGCAAGCAAACTCCAGAGCAAGTTTCTTA 240
 DB 61 SerAlaLeuLysSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
 DB 81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgGlu 40
 QY 301 ACTATGATTACGGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360
 DB 101 Thr---AlaThrLeuTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119
 QY 361 TCA 363
 DB 120 Ser 120

RESULT 4

; US-08-752-844-16
 ; Sequence 16, Application US/08752844
 ; Patent No. 5935821
 ; GENERAL INFORMATION:
 ; APPLICANT: Chatterjee, Malaya
 ; APPLICANT: Foon, Kenneth A.
 ; APPLICANT: Chatterjee, Sunil K.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
 ; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/752,844
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schiff, J. Michael
 ; REGISTRATION NUMBER: 40,253
 ; REFERENCE/DOCKET NUMBER: 30414-20002.21
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-752-844-16

Alignment Scores:
 Pred. No.: 2,99e-59 Length: 119
 Score: 535.00 Matches: 104
 Percent Similarity: 88.43% Conservative: 3
 Best Local Similarity: 85.95% Mismatches: 12
 Query Match: 79.49% Indels: 2
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-752-844-16 (1-119)

QY 1 CAGTGCAGCTCGAGAGTCTGGAGCTGGCTGGCTGGCGCCCTCACAGAGCTGTCCATC 60
 DB 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
 QY 61 ACTTGCACTGTCTGGGATTTCAATAACAGATATGTGTACACTGGGTTCGCCAGCCT 120
 DB 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
 QY 121 CCAGAAAGGCTCTGGAGTCTGGAGTAATATGAGTCTGGTGGGAGCACAATAATTAAT 180
 DB 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCTCATGTCAGACTCAGCAAGCAAACTCCAGAGCAAGTTTCTTA 240
 DB 61 SerAlaLeuLysSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
 DB 81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgGlu 100
 QY 301 ACTATGATTACGGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360
 DB 101 ***-----**TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 118
 QY 361 TCA 363
 DB 119 Ser 119
 RESULT 5

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US-08-591-196-16
; Sequence 16, Application US/08591196
; Patent No. 597316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: US/08/591,196
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-591-196-16

Alignment Scores:
Pred. No.: 2,99e-59 Length: 119
Score: 535.00 Matches: 104
Percent Similarity: 88.43% Conservative: 3
Best Local Similarity: 85.95% Mismatches: 12
Query Match: 79.49% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-591-196-16 (1-119)
QY 1 CAGGTGCAGCTCAGAGAGTCTGGAGCTGGCGCCCTCAGAGCCGTGTCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSer120
QY 61 ACTTCGACGTCTCTGGGATTTTCATTAACAGATATGTTACATGGGTTGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGGTGGAGTAATATGACTGGTGGAGCAACAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
QY 181 TGGCTCTCATGTCCAGATCGACATCAGCAAGACAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 ARAATCAAGACTGCAGACTGATCAGAGCCATGTAATCTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgGlu***** 100

US-08-591-196-16
; Sequence 16, Application US/08591196
; Patent No. 597316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 16-JAN-1996
; APPLICATION NUMBER: US/08/591,196
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-591-196-16

Alignment Scores:
Pred. No.: 2,99e-59 Length: 119
Score: 535.00 Matches: 104
Percent Similarity: 88.43% Conservative: 3
Best Local Similarity: 85.95% Mismatches: 12
Query Match: 79.49% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-293-533-16 (1-119)
QY 1 CAGGTGCAGCTCAGAGAGTCTGGAGCTGGCGCCCTCAGAGCCGTGTCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSer120
QY 61 ACTTCGACGTCTCTGGGATTTTCATTAACAGATATGTTACATGGGTTGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGGTGGAGTAATATGACTGGTGGAGCAACAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
QY 181 TGGCTCTCATGTCCAGATCGACATCAGCAAGACAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 ARAATCAAGACTGCAGACTGATCAGAGCCATGTAATCTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgGlu***** 100
```


STRANDEDNESS: single
TOPOLOGY: linear
US-08-973-518-4

Alignment Scores:

Pred. No.: 8,92e-59 Length: 140
Score: 531.50 Matches: 103
Percent Similarity: 88.43% Conservative: 4
Best Local Similarity: 85.12% Mismatches: 13
Query Match: 78.97% Indels: 1
DB: 3 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-973-518-4 (1-140)

QY 1 CAGGTGAGTGCAGGAGTCTGACCTGGCTGGTGGCGCCCTCAGAGCCTGTCCATC 60
DB 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40
QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTGCCAGCCT 120
DB 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60
QY 121 CCAGGAAGGCTCTGAGTGGCTGGAGTAATATGCACTGGTGGAGCACAATTTAAT 180
DB 61 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTrpAsn 80
QY 181 TCGGTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAAGAGCCAAAGTTTCTTA 240
DB 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPhelySerGlnValPheLeu 100
QY 241 AAATGAACAGTCTGAGACTGATGACAGCCATGTACTGTGCCAGAGATCGATCT 300
DB 101 LysMetSerSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120
QY 301 ACTATGATTAAGCCCTGATCTGACTGACTGGGGCCAGAGGACACCGTCACTCC 360
DB 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139
QY 361 TCA 363
DB 140 Ser 140

RESULT 9

5455030-15
PATENT NO. 5455030
APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
POLYPEPTIDE BINDING MOLECULES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
SEQ ID NO: 15:
LENGTH: 242
5455030-15

Alignment Scores:

Pred. No.: 2,02e-58 Length: 242
Score: 529.50 Matches: 103
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 85.83% Mismatches: 11
Query Match: 78.68% Indels: 1
DB: 6 Gaps: 1

US-10-049-868A-2 (1-363) x 5455030-15 (1-242)
QY 4 GTGACGTGAGGAGTCTGACCTGGCTGGTGGCGCCCTCAGAGCCTGTCCATCACT 63
DB 124 ValGlnLeuLysGluSerGlyProValLeuValAlaProSerGlnSerLeuSerIleThr 143
QY 64 TGCACCTGCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTGCCAGCCTCCA 123
DB 144 CysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnProPro 163
QY 124 GGAAGGCTCTGAGTGGCTGGAGTAATATGCACTGGTGGAGGACCAATTAATATTCG 183
DB 164 GlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlyAsnThrAsnTyrAsnSer 183
QY 184 GCTCTCATCTCAGACTGAGCATCAGCAAGACAACTCCAAAGAGCCAAAGTTTCTTAAA 243
DB 184 AlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysGlnValPheLeuLys 203
QY 244 ATGAACAGTCTGACACTGATGACAGCCATGTACTGTGCCAGAGATCGATCTACT 303
DB 204 MetAsnSerLeuGlnIleAspThrAlaIleTyrTyrCysAlaLys---ArgLeuGlu 222
QY 304 ATGATTAAGGCTGCTGCTGACTGACTGGGGCCAGAGGACACCGTCACTCCCTCA 363
DB 223 ArgIlePheTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 242

RESULT 10

US-08-881-037-67
Sequence 67, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-67
Alignment Scores: 4.84e-58 Length: 121
Pred. No.:

Score: 525.50 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 14
Query Match: 78.08% Indels: 1
DB: 3 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-881-037-67 (1-121)

QY 1 CAGGTGCAGCTCAGAGCTCGGAGCTGGCTGGGCGCCCTCAGAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLeuGlySerGlyProValLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTGGGATTTTCATTAACAGATATGGTGACACTGGGTTCCGCCAGCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGAAAGGGTCTGGAGTGGCTGGAGTAATATGCACTGGTGGAGGACCAAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGAGTCAGATCAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTCATCACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaLysHisLeuPro 100
QY 301 ---ACTATGATTAACGGCTATGCTATGAGTACTGGGCGCAAGGACCAAGCTCCCGTC 357
Db 101 TyrGlyAsnTyrGlyTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrVal 120
QY 358 TCC 360
Db 121 Ser 121

RESULT 11
US-08-667-769A-15
; Sequence 15, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,769A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082
; FILING DATE: 22-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110

; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5030
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-667-769A-15

Alignment Scores:
Pred. No.: 9,98e-58 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 1 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-667-769A-15 (1-119)

QY 1 CAGGTGCAGCTCAGAGCTCGGAGCTGGCTGGGCGCCCTCAGAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTGGGATTTTCATTAACAGATATGGTGACACTGGGTTCCGCCAGCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValArgGlnPro 40
QY 121 CCAGAAAGGGTCTGGAGTGGCTGGGAGTAATATGCACTGGTGGAGGACCAAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
QY 181 TCGGCTCTCATGTCAGAGTCAGATCAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTCATCACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspProPro 100
QY 301 ACTATGATTAACGGCTATGCTATGAGTACTGGGCGCAAGGACCAAGCTCCCGTC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 12
PCT-US95-17082A-15
; Sequence 15, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.

;; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
;; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
;; NUMBER OF SEQUENCES: 76
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: SmithKline Beecham Corp./Corporate

;; STREET: P.O. Box 1539-UW2220

;; CITY: King of Prussia

;; STATE: Pennsylvania

;; COUNTRY: USA

;; ZIP: 19406-0939

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US95/17082A

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/470110

;; FILING DATE: 06-JUN-1995

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/467420

;; FILING DATE: 06-JUN-1995

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/363131

;; FILING DATE: 23-DEC-1994

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Sutton, Jeffrey A.

;; REGISTRATION NUMBER: 34,028

;; REFERENCE/DOCKET NUMBER: P50282-2

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 610-270-5024

;; TELEFAX: 610-270-5090

;; INFORMATION FOR SEQ ID NO: 15:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 119 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

PCT-US95-17082A-15

Alignment Scores:
Pred. No.: 9,98e-58 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 5 Gaps: 1

US-10-049-868a-2 (1-363) x PCT-US95-17082A-15 (1-119)

QY 1 CAGGTGACGTGACGAGGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGACGTCTCTGGGATTCATTAAACAGATATGGTGACACTGGGTGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGAGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGACCAATTAAT 180
Db 41 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGATGACATCAGCAAAAGACAATCCAAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AATGACAGTCTGACAGTCTGATGACAGCCATGTACTGTCTGCCAGATCCATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspProPro 100

QY 301 ACTATGATTACGGCCTATGCTATGACTACTGGGGCCAAAGGACACGCTCACCGTCTCC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 13

US-09-189-129-3

;; Sequence 3, Application US/09189129

;; Patent No. 6323027

;; GENERAL INFORMATION:

;; APPLICANT: Burkly, Linda C

;; APPLICANT: Benjamin, Christopher D

;; APPLICANT: Hession, Catherine A

;; APPLICANT: Whitty, Adrian

;; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS

;; NUMBER OF SEQUENCES: 17

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Biogen, Inc.

;; STREET: 14 Cambridge Center

;; CITY: Cambridge

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02142

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/189,129

;; FILING DATE:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: A006 PCT CIP

;; FILING DATE: 09-MAY-1997

;; APPLICATION NUMBER: 60/017,466

;; FILING DATE: 10-MAY-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Kaplan, Warren A.

;; REGISTRATION NUMBER: 34,199

;; REFERENCE/DOCKET NUMBER: A006 PCT CIP

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 617 679-2000

;; TELEFAX: 617 679-2838

;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 112 amino acids

;; TYPE: amino acid

;; STRANDEDNESS:

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; FRAGMENT TYPE: internal

US-09-189-129-3

Alignment Scores:
Pred. No.: 1,51e-57 Length: 112
Score: 521.50 Matches: 98
Percent Similarity: 92.11% Conservative: 8
Best Local Similarity: 85.22% Mismatches: 6
Query Match: 77.49% Indels: 3
DB: 3 Gaps: 1

US-10-049-868a-2 (1-363) x US-09-189-129-3 (1-112)

QY 10 CTGCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATCCTTGCCT 69
Db 1 LeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThr 20
QY 70 GTCTCTGGGATTCATTAAACAGATATGGTGACACTGGTTCGCCAGCCTCCAGGAAG 129

Db 21 ValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLys 40
 QY 130 GGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCCCTCAGACAGCCCTGTCCATCCTGCCTC 189
 Db 41 GlyLeuGlnTrpLeuGlyValIleTrpAlaGlySerThrAsnTyrAsnSerAlaLeu 60
 QY 190 ATGTCAGACTGAGCATCAGCAAAACAGCAACTCCAGAGCCAAAGTTTCTTAAATAATGAAC 249
 Db 61 MetSerArgLeuAsnIleAsnArgAspAsnSerLysSerGlnIlePheLeuLysMetAsn 80
 QY 250 AGTCTGCAGACTGATGACACAGCCATGACTACTGTGCGCAGAGATCGATCTACTATGATT 309
 Db 81 SerLeuGlnThrAspAspThrAlaIleTyrTyrCysAlaArgGluGlySerThrVal--- 99
 QY 310 ACGGCCTATGCTATGGACTGGGGCCCAAGGACCAAGGACCGGTCAAC 354
 Db 100 -----AspSerMetAspTyrTrpGlyGlnGlyThrValThr 112

RESULT 14

US-09-824-286-3
 ; Sequence 3, Application US/09824286
 ; Patent No. 6770745
 ; GENERAL INFORMATION:
 ; APPLICANT: Burkly, Linda C
 ; Benjamin, Christopher D
 ; Hession, Catherine A
 ; Whitty, Adrian
 ; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Biogen, Inc.
 ; STREET: 14 Cambridge Center
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02142
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/824,286
 ; FILING DATE: 02-Apr-2001
 ; CLASSIFICATION: <unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/017,466
 ; FILING DATE: 10-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaplan, Warren A.
 ; REGISTRATION NUMBER: 34,199
 ; REFERENCE/DOCKET NUMBER: A006 PCT CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617 679-2000
 ; TELEFAX: 617 679-2838
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 112 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-824-286-3

Alignment Scores:
 Pred. No.: 1,51e-57 Length: 112
 Score: 521.50 Matches: 98
 Percent Similarity: 92.17% Conservatives: 8
 Best Local Similarity: 85.22% Mismatches: 6
 Query Match: 77.49% Indels: 3
 DB: 4 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-824-286-3 (1-112)
 QY 10 CTGACAGAGTCTGAGCCTGGCTGGCTGGTGGCCCTCAGACAGCCCTGTCCATCCTGCCTC 69
 Db 1 LeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThr 20
 QY 70 GTCTCTGGGATTTTCATTAACAGATATGGTGTACACTGGGTTCGCCAGCCTCCAGGAAG 129
 Db 21 ValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLys 40
 QY 130 GGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCCCAAAATTAATAATCGGCTCTC 189
 Db 41 GlyLeuGlnTrpLeuGlyValIleTrpAlaGlySerThrAsnTyrAsnSerAlaLeu 60
 QY 190 ATGTCAGACTGAGCATCAGCAAAACAGCAACTCCAGAGCCAAAGTTTCTTAAATAATGAAC 249
 Db 61 MetSerArgLeuAsnIleAsnArgAspAsnSerLysSerGlnIlePheLeuLysMetAsn 80
 QY 250 AGTCTGCAGACTGATGACACAGCCATGACTACTGTGCGCAGAGATCGATCTACTATGATT 309
 Db 81 SerLeuGlnThrAspAspThrAlaIleTyrTyrCysAlaArgGluGlySerThrVal--- 99
 QY 310 ACGGCCTATGCTATGGACTGGGGCCCAAGGACCAAGGACCGGTCAAC 354
 Db 100 -----AspSerMetAspTyrTrpGlyGlnGlyThrValThr 112

RESULT 15
 US-08-860-174A-2
 ; Sequence 2, Application US/08860174A
 ; Patent No. 5989830
 ; GENERAL INFORMATION:
 ; APPLICANT: DAVIS, Paul James
 ; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
 ; APPLICANT: VERHOEIJEN, Martine Elisa
 ; APPLICANT: WILSON, Steve
 ; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
 ; ANTI-BODY FRAGMENT ANALOGUE
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: PILLSBURY, MADISON & SUTRO LLP
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington, D.C.
 ; STATE:
 ; COUNTRY: UNITED STATES
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
 ; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/860,174A
 ; FILING DATE: June 16, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95307332.7
 ; FILING DATE: October 16, 1995
 ; APPLICATION NUMBER: PCT/EP/96/03605
 ; FILING DATE: August 14, 1996
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 239 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-860-174A-2

Alignment Scores:
 Pred. No.: 6,69e-57 Length: 239
 Score: 517.50 Matches: 100
 Percent Similarity: 87.60% Conservatives: 6
 Best Local Similarity: 82.64% Mismatches: 10

```
Query Match:      76.83%      Indels:      5
DB:                2              Gaps:      1
US-10-049-868A-2 (1-363) x US-08-860-174A-2 (1-239)

QY 1 CAGGTGCAGCTCAGAGTCTGGACCTGGCTGGTGGGCCCTCAGAGCCTGTCCATC 60
Db 124 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 143
QY 61 ACTTGCACTCTCTCTGGGATTTTCATTAAACAGATATGGTGATCACTGGSTTCGCCAGCCT 120
Db 144 ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAsnTrpValArgGlnPro 163
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAAATATGGACTGGTGGAGCACAATATATAT 180
Db 164 ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlyAsnThrAspTyrAsn 183
QY 181 TCGGCTCTCANTCCAGACTGAGCATCAGCAAGCAACTCCAGAGCCCAAGTTTCTTTA 240
Db 184 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 203
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGAGCATGTACTACTGTCACAGATCGATCT 300
Db 204 LysMetAsnSerLeuHisThrAspAspThrAlaArgTyrTyrCysAlaArgGluArgAsp 223
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCCAAGGGACCACGGTCACCGTCTCC 360
Db 224 -----TyrArgLeuAspTyrTrpGlyGlnGlyThrThrValThrValSer 238
QY 361 TCA 363
Db 239 Ser 239
```

Search completed: October 13, 2004, 13:31:12
Job time : 22.8705 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:12:25 ; Search time 21.3809 Seconds

(without alignments)
3231.093 Million cell updates/sec

Title: US-10-049-868A-1

Perfect score: 674

Sequence: 1 gacattgagctcaccagctc.....gtatccattcttcagcttcc 359

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10049868/runat_13102004_132817_24805/app_query.fasta_1.1038
-DB=pir_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 -CGEN 1 1 77 @runat_13102004_132817_24805 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGSEQQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	460	68.2	235	2	IG kappa chain - m
2	448	66.5	140	2	IG kappa chain pre
3	437	64.8	107	2	IG kappa chain v r
4	427	63.4	130	1	IG kappa chain pre
5	422	62.6	106	2	IG light chain v r
6	422	62.6	107	2	IG kappa chain v r
7	420	62.3	107	2	IG kappa chain v r
8	419	62.2	103	2	IG kappa chain v r
9	419	62.2	132	2	IG kappa chain pre
10	417	61.9	106	2	IG kappa chain v r
11	417	61.9	107	2	IG kappa chain v r
12	416	61.7	106	2	IG kappa chain v r
13	415	61.6	104	2	IG kappa chain v r
14	413	61.3	107	2	IG kappa chain v r

15	411	61.0	107	2	S11118	IG kappa chain v r
16	405	60.1	107	2	S11121	IG kappa chain v r
17	402.5	59.7	108	2	G30560	IG kappa chain v r
18	401	59.5	107	2	P70406	IG kappa chain v r
19	400	59.3	107	2	P70403	IG light chain v r
20	399	59.2	107	2	S11112	IG kappa chain v r
21	398	59.1	107	2	S11117	IG kappa chain v r
22	396	58.8	107	2	P70398	IG light chain v r
23	394	58.5	104	2	JC6076	anti-D-dimer monoc
24	392	58.2	107	2	P70402	IG light chain v r
25	390	57.9	100	2	S29590	IG kappa chain v r
26	389.5	57.8	106	2	S11114	IG kappa chain v r
27	389	57.7	130	2	B32456	IG kappa chain pre
28	386	57.3	107	2	P70401	IG light chain v r
29	385	57.1	106	2	PS0070	IG kappa chain v r
30	385	57.1	120	2	A34871	IG kappa chain v r
31	384	57.0	97	2	PH1084	IG light chain v r
32	384	57.0	107	2	S11113	IG kappa chain v r
33	384	57.0	107	2	P70395	IG light chain v r
34	384	57.0	130	2	S04573	IG kappa chain pre
35	382	56.7	97	2	S26341	IG light chain v r
36	382	56.7	107	2	S11116	IG kappa chain v r
37	382	56.7	107	2	P70400	IG light chain v r
38	382	56.7	107	2	A42848	IG light chain v r
39	380	56.4	107	2	S11123	IG kappa chain v r
40	379	56.2	107	1	KVMSX4	IG kappa chain v r
41	376.5	55.9	145	2	PL0014	IG kappa chain pre
42	376	55.8	105	2	S26338	IG kappa chain v r
43	376	55.8	107	2	P70397	IG light chain v r
44	376	55.8	130	2	A32513	IG kappa chain pre
45	373	55.3	120	2	S66536	IG light chain v r

ALIGNMENTS

RESULT 1

S25058

IG kappa chain - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C/Accession: S25058

R/Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific

A/Reference number: S25057

A/Accession: S25058

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-235 <FIS>

A/Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829

C/Superfamily: immunoglobulin v region; immunoglobulin homology

F:38-111/Domain: immunoglobulin homology <IMV>

Alignment Scores:				
Pred. No.:	2.29e-35	Length:	235	
Score:	460.00	Matches:	92	
Percent Similarity:	85.34%	Conservative:	7	
Best Local Similarity:	79.31%	Mismatches:	17	
Query Match:	68.25%	Indels:	0	
DB:	2	Gaps:	0	

US-10-049-868A-1 (1-359) x S25058 (1-235)

Qy	4	ATTGAGTCACCCAGTCTCCAGCAATCATGTGTGATCTCCAGGGAGAGGTCCACCATG	63
Db	24	IleValLeuthrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet	43
Qy	64	ACCTGCAGTCCAGTTCAGTGTAAATATGACATGCTTCAGCAGGAGTCCGGCACC	123
Db	44	ThrCysSerAlaSerSerValSerLysMetGlnTrpTrpGlnGlnLysSerGlyThr	63
Qy	124	TTCCCCAAAAGAGGATTTATGACATCCAACTGCTTCTGGAGTCCCTGCTCGCCTC	183

Db 64 SerProLysArgTyrTrpIleTyrAspThrSerLysLeuAlaSerGlyValProGlyArgPhe 83
 QY 184 ACTGGAGTGGTCTGGGACAGAAATCCACCTCGGAATCAGTAGAGTGAAGCTAGGAT 243
 Db 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 103
 QY 244 GTGGGTGTATTACTGTCAACAACTGTGTAGAGTATCCGCTCAGCTTGGTCTGGGACC 303
 Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 123
 QY 304 AAGCTGGAGCTGAAGGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
 Db 124 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 139

RESULT 2

PL0013
 Ig kappa chain precursor V region (4C11) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: PL0013

R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988
 A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: PL0011; PMID:88142863; PMID:3125424
 A:Accession: PL0013

A:Molecule type: mRNA
 A:Residues: 1-140 <CHE>

A:Experimental source: cell line 4C11
 C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:46-55/Region: complementarity-determining 1
 F:71-77/Region: complementarity-determining 2
 F:110-118/Region: complementarity-determining 3
 F:130-140/Domain: constant region (fragment) #status predicted <COR>

Alignment Scores:

Pred. No.: 3,22e-34 Length: 140
 Score: 448.00 Matches: 88
 Percent Similarity: 82.76% Conservative: 8
 Best Local Similarity: 75.86% Mismatches: 20
 Query Match: 66.47% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x PL0013 (1-140)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCCACATG 63
 Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIle 43
 QY 64 ACCTGCAGTCCAGTTCAGTGTAAATACATCATCTGCTCCAGCAGGAGTGGGCACC 123
 Db 44 ThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysProAspThr 63
 QY 124 TTCGCCAAAGAGAGATTATGACACATCCAACTGCTTCTGGAGTCCCTGCTGCCTC 183
 Db 64 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProValArgPhe 83
 QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTCGGAATCAGTAGAGTGAAGCTGAGGAT 243
 Db 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAsp 103
 QY 244 GTGGGTGTATTACTGTCAACAACTGTGTAGAGTATCCGCTCAGCTTGGTCTGGGACC 303
 Db 104 AlaAlaThrTyrTyrCysGlnGlnArgSerSerTyrProProThrPheGlyGlyThr 123
 QY 304 AAGCTGGAGCTGAAGGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
 Db 124 LysLeuGluMetLysArgAlaAspAlaAlaProThrValSerIlePhe 139

RESULT 3

PC4405
 Ig kappa chain V region (F3, anti-APP) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
 C:Accession: PC4405

R:Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
 Chinese Biochem. J. 12, 648-653, 1996
 A:Title: Generation of a phage display library of the immunoglobulin repertoire from hu

A:Reference number: PC4405
 A:Accession: PC4405
 A:Molecule type: mRNA
 A:Residues: 1-107 <DEN>
 A:Cross-references: UNIPROT:Q8K1F0
 A:Experimental source: spleen cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 3,57e-33 Length: 107
 Score: 437.00 Matches: 84
 Percent Similarity: 86.92% Conservative: 9
 Best Local Similarity: 78.50% Mismatches: 14
 Query Match: 64.84% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x PC4405 (1-107)

QY 1 GACATTGAGTCCACAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCCACC 60
 Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
 QY 61 ATGACCTGCAGTCCAGTTCAGTGTAAATACATCATCTGCTCCAGCAGGAGTGGGC 120
 Db 21 MetThrCysSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGly 40
 QY 121 ACCTTCCCCAAAGAGGATTTATGACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
 Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
 QY 181 CTCAGTGCAGTGGTCTGGGACAGAAATTCACCTCGGAATCAGTAGAGTGAAGGTGAG 240
 Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgValGluAlaGlu 80
 QY 241 GATGTGGGTGTATTACTGTCAACACTTGTAGAGTATCCGCTCAGCTTGGTCTGGG 300
 Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpArgAspAsnProProThrPheGlyGly 100
 QY 301 ACCAAGCTGGAGCTGAACCGG 321
 Db 101 ThrLysLeuGluIleLysArg 107

RESULT 4

JL0079
 Ig kappa chain precursor V region (anti-phenylloxazolone 6F6) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
 C:Accession: JL0079; A49044; E49044

R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
 Mol. Immunol. 25, 859-865, 1988
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re

A:Reference number: JL0076; PMID:89096973; PMID:3211160
 A:Accession: JL0079

A:Molecule type: mRNA

A:Residues: 1-130 <KAA>

A:Cross-references: GB:M27792; NID:g197159

A:Experimental source: mRNA clones for anti-phenylloxazolone antibody 6F6

A:Note: The authors translated the codon TTC for residue 8 as Pro and TTC for residue
 A:Note: the codon given for I-Met (AGT) is inconsistent with the authors' translation
 R:Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
 Eur. J. Immunol. 22, 1627-1634, 1992

A:Title: Non-random features of the repertoire expressed by the members of one V kappa

A:Reference number: A49044; PMID:92289826; PMID:1601044

A:Accession: A49044
 A:Molecule type: DNA
 A:Residues: 1-25 <MTL>
 A:Cross-references: GB:S37663; NID:q250214; PIDN:AAB22331.1; PID:q250217
 A>Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
 A:Accession: B49044
 A:Molecule type: DNA
 A:Residues: 114-116 <MTL2>
 A:Cross-references: GB:S37664; NID:q250215; PIDN:AAB22332.1; PID:q250218
 A:Experimental source: BAMB/c germ-line
 A>Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional disulfide bonds
 C:Genetics:
 A:Gene: V(kappa)Ox1
 A:Introns: 17/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:45-109/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 3,07e-32 Length: 130
 Score: 427.00 Matches: 84
 Percent Similarity: 85.0% Conservative: 7
 Best Local Similarity: 78.50% Mismatches: 16
 Query Match: 63.35% Indels: 0
 DB: 1 Gaps: 0

US-10-049-868A-1 (1-359) x JLU0079 (1-130)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAGGTCCACCATG 63
 DB 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43

QY 64 ACCTGCAGTGCAGTTCAGTGAATTAATACATGCACTGTTCCAGCAGGAGTCGGGCACC 123
 DB 44 ThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysSerGlyThr 63

QY 124 TTCCTCCAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
 DB 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 83

QY 184 AGTGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTCAGGAT 243
 DB 84 SerGlySerGlySerGly***SerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 103

QY 244 GTGGGTGTGTATTACTGTCAACAACTGTAGAGTATCCGCTCACGTTCCGTTGCTGGGACC 303
 DB 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 123

QY 304 AAGCTGGAGCTGAACGGGCT 324
 DB 124 LysLeuGlu***LysArgAla 130

RESULT 5
 B54378
 Ig light chain V region anti-triplex DNA - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B54378
 R:Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
 J. Biol. Chem. 269, 7019-7023, 1994
 A:Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
 A:Reference number: A54378; MUID:94165109; PMID:7509814
 A:Accession: B54378
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-106 <AGA>
 A:Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747

A:Experimental source: spleen and myeloma cell line MOPC 315.43
 A>Note: sequence inconsistent with nucleotide translation
 A:Residues: 1-141 <MTL>
 A:Cross-references: GB:S37663; NID:q250214; PIDN:AAB22331.1; PID:q250217
 A>Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 9,22e-32 Length: 106
 Score: 422.00 Matches: 82
 Percent Similarity: 85.71% Conservative: 8
 Best Local Similarity: 78.10% Mismatches: 15
 Query Match: 62.61% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x B54378 (1-106)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAGGTCCACCATG 63
 DB 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIle 21

QY 64 ACCTGCAGTGCAGTTCAGTGAATTAATACATGCACTGTTCCAGCAGGAGTCGGGCACC 123
 DB 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThr 41

QY 124 TTCCTCCAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
 DB 42 SerProLysLeuTrpIleTyrSerThrSerLysLeuAlaSerGlyValProAlaArgPhe 61

QY 184 AGTGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTCAGGAT 243
 DB 62 SerGlySerGlySerGlyThrSerTyrSerLeuProIleSerArgMetGluAlaGluAsp 81

QY 244 GTGGGTGTGTATTACTGTCAACAACTGTAGAGTATCCGCTCACGTTCCGTTGCTGGGACC 303
 DB 82 AlaAlaThrTyrTyrCysGlnGlnArgSerSerTyrProIleThrPheGlyAlaGlyThr 101

QY 304 AAGCTGGAGCTGAAC 318
 DB 102 LysLeuGluLeuLys 106

RESULT 6
 A30562
 Ig kappa chain V regions (27, 7.2 and 27.4b.2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
 C:Accession: A30562
 R:Sikder, S.K.; Borden, P.; Grzeszo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.
 J. Immunol. 142, 888-893, 1989
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
 A:Reference number: A30562; MUID:89110066; PMID:2464031
 A:Accession: A30562
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
 Pred. No.: 9,21e-32 Length: 107
 Score: 422.00 Matches: 82
 Percent Similarity: 84.91% Conservative: 8
 Best Local Similarity: 77.36% Mismatches: 16
 Query Match: 62.61% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x A30562 (1-107)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAGGTCCACCATG 63
 DB 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21

QY 64 ACCTGAGTGCAGTTCAGTGTATTAATACATGCTGCTCCAGCAGGAGTGGGCACC 123

Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41

QY 124 TTCCCAAGAGAGATTTATGACATCCAAATGGCTTCTGGAGTCCCTGCTGCCTC 183

Db 42 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 61

QY 184 ACTGGCAGTGGTCTGGGACAGAAATCACCTCGGAATCAGTAGAGTGAAGCTGAGAT 243

Db 62 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 81

QY 244 GTGGGTGTATTAATGTCACAACTGATCCGCTCAGGTCCTGGTCTGGGACC 303

Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProTyrThrPheGlyGlyGlyThr 101

QY 304 AAGCTGGAGCTGAACGG 321

Db 102 LysLeuGluIleLysArg 107

RESULT 7

PD0011

Ig kappa chain V region (VUB10, anti-AFP) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000

C:Accession: PD0011

R:Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.

Chinese Biochem. J. 12, 648-653, 1996

A:Reference: Generation of a phage display library of the immunoglobulin repertoire from hum

A:Contents: Spleen

A:Accession: PD0011

A:Molecule type: mRNA

A:Residues: 1-107 <EN>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1-42e-31 Length: 107

Score: 420.00 Matches: 82

Percent Similarity: 85.98% Conservative: 10

Best Local Similarity: 76.64% Mismatches: 15

Query Match: 62.31% Indels: 0

DB: 2 Gaps: 0

US-10-049-868a-1 (1-359) x PD0011 (1-107)

QY 1 GACATTGAGTCCAGTTCAGCAATCATCTGCAATCTCCAGGGAGAGGTCAAC 60

Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY 61 ATCACTGAGTCCAGTTCAGTGTATTAATACATGCTGCTCCAGCAGGAGTGGGC 120

Db 21 MetTyrSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGly 40

QY 121 ACCTTCCCAAGAGAGATTTATGACATCCAAATGGCTTCTGGAGTCCCTGCTGC 180

Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaLys 60

QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTCGGAATCAGTAGAGTGAAGCTGAG 240

Db 61 GlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerArgValGluAlaGlu 80

QY 241 GATGTGGTGTATTAATGTCACAACTGATCCGCTCAGGTCCTGGTCTGGG 300

Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpArgAsnProProThrProGlyGlyGly 100

QY 301 ACCAAGCTGAGCTGAACGG 321

Db 101 ThrLysLeuGluIleLysArg 107

RESULT 8

S29591

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S29591

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S29591

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-103 <NAV>

A:Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-88/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.77e-31 Length: 103

Score: 419.00 Matches: 82

Percent Similarity: 86.41% Conservative: 7

Best Local Similarity: 79.61% Mismatches: 14

Query Match: 62.17% Indels: 0

DB: 2 Gaps: 0

US-10-049-868a-1 (1-359) x S29591 (1-103)

QY 4 ATTGAGTCCAGTTCAGCAATCATCTGCAATCTCCAGGGAGAGGTCAACATG 63

Db 1 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 20

QY 64 ACCTGAGTCCAGTTCAGTGTATTAATACATGCTGCTCCAGCAGGAGTGGGCACC 123

Db 21 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 40

QY 124 TTCCCAAGAGAGATTTATGACATCCAAATGGCTTCTGGAGTCCCTGCTGCCTC 183

Db 41 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 60

QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTCGGAATCAGTAGAGTGAAGCTGAGGAT 243

Db 61 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 80

QY 244 GTGGGTGTATTAATGTCACAACTGATCCGCTCAGGTCCTGGTCTGGGACC 303

Db 81 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 100

QY 304 AAGCTGGAG 312

Db 101 LysLeuGlu 103

RESULT 9

S05268

Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000

C:Accession: S05268; J10062; S03846

R:Levy, S.

submitted to the EMBL Data Library, February 1989

A:Reference number: S05267

A:Accession: S05268

A:Molecule type: mRNA

A:Residues: 1-132 <LEV>

A:Cross-references: EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261

R:Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.

J. Exp. Med. 168, 1607-1620, 1988

A:Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An expla

A:Reference number: J10061; MUID:89035985; PMID:3141553

A:Accession: J10062

A:Molecule type: mRNA

A:Residues: 1-120 <CAR>

A:Cross-references: EMBL:X14098

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

QY 64 ACCTGCAGTGCCAGTTCAGTGTTAATACATGCAC TGCTCCAGCAGGAGTCGGGGCAC 123

RESULT
G27887

A;Accession: J00000
A;Accession: J00000
A;Accession: J00000
A;Molecule type: DNA
A;Residues: 1-106 <CAT>
A;Cross-references: UNIPROT:Q8VDDO
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMW>

[illegible]

```

DB      82 AAlAAAHMHYIYYCYSGHGHGHHHPSEIRASHPFTELEUHFNEGYALAGRIYIN
QY      304 AAGCTGGAG 312
        |||||
DB      102 LysLeuGlu 104
        |||||

RESULT 14
Sll119
IG kappa chain V region (clone NO6-8.3.1) ~ mouse (fragment)
C/SPECIES: Mus musculus (house mouse)
C/DATE: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C/ACCESSION: Sll119
R/Kaarinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1993
A/TITLE: mRNA sequences define an unusually restricted IgG response to 2-pheny
A/REFERENCE NUMBER: S07331; UID:832711467; PMID:6877353
A/ACCESSION: Sll119
A/Molecule type: mRNA
A/Residues: 1-107 <NAT>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
P:16-89/Domain: immunoglobulin homology <IMM>
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Score:	415.00	Matches:	61
Percent Similarity:	82.08%	Conservative:	6
Best Local Similarity:	76.42%	Mismatches:	19
Query Match:	61.28%	Indels:	0
DB:	2	Gaps:	0

US-10-049-868A-1 (1-359) x S11119 (1-107)

Qy	4	ATTGAGCTCACCAGTCTCCAGCAATCATGTGTGCATCTCCAGGGAGAAAGGTCAACCATG	63
Db	2	IleValLeuThrGlnSerPro***IleMetSer***SerProGlyGluLysValThrMet	21
Qy	64	ACCTGAGTGCAGTTCAAAGTGTAAATTACATGACTGGTTCAGCAGGAGTCCGGGACC	123
Db	22	ThrCysSerAlaSerSerValSerTyrMethIstIrpTyrGlnGlnLysSerGlyThr	41
Qy	124	TTCCCCAAAGAGGATTATCAACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGGCTC	183
Db	42	SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe	61
Qy	184	AGTGGCAGTGGGTCTGGGCACAAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT	241

```
Db      62 SerGly**Gly**GlyThrSerTyrSerLeuThrIleSerSerMetPheAlaGluAsp 81
Qy      244 GTGGGTGTGATCTACTCAACAACTGTGTAGATCCGCTCAGTTCGGTGGTGGACC 303
Db      82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
Qy      304 AAGCTGGAGCTGAACGG 321
Db      102 LysLeuGluLeuLysArg 107

RESULT 15
S1118
Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C/Accession: S11118
R/Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A/Reference number: S07331; MUID:83271467; PMID:6877353
A/Accession: S1118
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <KAA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:      9.99e-31      Length:      107
Score:          411.00      Matches:      82
Percent Similarity: 83.02%      Conservative: 6
Best Local Similarity: 77.36%      Mismatches: 18
Query Match:    60.98%      Indels:      0
DB:              2          Gaps:          0

US-10-049-868A-1 (1-359) x S11118 (1-107)

Qy      4  ATTGAGTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCAACCATG 63
Db      2  ileValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21
Qy      64  ACCTGCAGTGCAGTCAAGTGTAAATTACATGCACCTGGTTCACAGCAGGAGTCGGGCACC 123
Db      22  ThrCysSerAlaSerSerSerValSerTyrMethIstTrpTyrGlnGlnLysSerGlyThr 41
Qy      124  TTCGCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGAGTCCCTCGCTCGCCTC 183
Db      42  SerProLysArgTrpIleTyrAspThrSerLysLeuAspSerGlyValProAlaArgPhe 61
Qy      184  AGTGGCAGTGGTGGTGGACAGAAATTCACCTGGAAATCAGTAGAGTCAAGGCTGAGGAT 243
Db      62  SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetPheAlaGluAsp 81
Qy      244  GTGGGTGTGATTAATCTGTCAACAACTGTGAGATATCCGCTCAGTTCGGTGGTGGACC 303
Db      82  AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
Qy      304  AAGCTGGAGCTGAACGG 321
Db      102  LysLeu**Leu***Arg 107
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Search completed: October 13, 2004, 13:29:37
Job time : 23.3809 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:01:14 ; Search time 103.175 Seconds
(without alignments)
4004.053 Million cell updates/sec

Title: US-10-049-868a-1

Perfect score: 674

Sequence: 1 gacatgagctaccacccagtc.....gtatccattcttcaggttcc 359

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p_model -DEV=xlbp
-Q=/cgm2_1/USPTO_spool_p/US10049868/runat_13102004_132817_24791/app_query.fasta_1.1038
-DB=UniProt_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868_@CGN_1_1_305_@runat_13102004_132817_24791 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCKS=100 -LONGIOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	452	67.1	112	2	Q8K1F2 mus muscu
2	451	66.9	235	2	Q91W12 mus muscu
3	444	65.9	134	2	Q8VDD0 mus muscu
4	433	64.2	112	2	Q8K1F0 mus muscu
5	421	62.5	107	1	KV6F MOUSE
6	419	62.2	112	2	Q8K1F3 mus muscu
7	419	62.2	114	2	Q8K1F1 mus muscu
8	416	61.7	107	1	KV6H MOUSE
9	415	61.6	107	1	KV6H MOUSE
10	415	61.6	235	2	Q7TWK0 mus muscu
11	414	61.4	107	1	KV6G MOUSE
12	411	61.0	111	2	AAR10981 mus muscu
13	411	61.0	111	2	AAR10982 mus muscu
14	411	61.0	111	2	AAR10994 mus muscu
15	410	60.8	108	2	AAR11048 mus muscu
16	409	60.7	110	2	AAR10999 mus muscu

17	408	60.5	107	1	KV6J MOUSE
18	398	59.1	107	2	AAR11015
19	392	58.2	106	2	Q9U410
20	386	57.3	108	1	KV6K MOUSE
21	385	57.1	107	1	KV6C MOUSE
22	380	56.4	107	1	KV6B MOUSE
23	379.5	56.3	214	2	Q91A5
24	379	56.2	107	1	KV6A_MOUSE
25	379	56.2	107	1	KV6D_MOUSE
26	377	55.9	111	2	AAR11009
27	374	55.5	106	2	AAR11006
28	373.5	55.4	236	2	Q7TS98
29	370	54.9	107	1	KV6E_MOUSE
30	368.5	54.7	131	2	Q811C3
31	366	54.3	97	2	AAR11055
32	364	54.0	92	2	AAR11066
33	364	54.0	95	2	AAR11062
34	360.5	53.5	114	2	AAR10983
35	358.5	53.2	234	2	Q8R062
36	358	53.1	111	2	AAR11021
37	356.5	52.9	234	2	Q8VCP0
38	355.5	52.7	237	2	Q7S236
39	354	52.5	129	1	KV4A_MOUSE
40	353.5	52.4	236	2	Q7Z3Y4
41	350.5	52.0	112	2	AAR11019
42	347.5	51.6	114	2	AAR11022
43	347.5	51.6	236	2	Q6PIH7
44	347.5	51.6	236	2	Q6GMX9
45	347.5	51.6	236	2	AAH34141

ALIGNMENTS

RESULT 1

Q8K1F2 PRELIMINARY; PRT; 112 AA.

AC Q8K1F2;

DT 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Anti-Virase light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Plaque S., Karle S., Nishiyama Y., Paul S.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF516283; AAM64201.1; -

DR PIR; H39332; H39332.

DR HSSP; Q91W12; 1AY1.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF000047; ig_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 112

SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;

Alignment Scores:

Pred. No.: 1.27e-41 Length: 112
Score: 452.00 Matches: 88
Percent Similarity: 85.71% Conservative: 8
Best Local Similarity: 78.57% Mismatches: 16
Query Match: 67.06% Indels: 0
DB: 2 Gaps: 0

US-10-049-868a-1 (1-359) x Q8K1F2 (1-112)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGCTCTGATCTCCAGGGGAGGTCCACC 60

Db	1	AspIleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluValThr	20
Qy	61	ATGACCTGCAGTGCAGTTCAGGTGAATACATGCAGTGGTCCACGAGGAGTCGGGC	120
Db	21	IleThrCysAsnAlaSerSerValSerTyrMetHisTrrpPheGlnGlnIlysProGly	40
Qy	121	ACCTTCCCCAAAAGAAGATTATGACACATCCAACTGGCTTCTGGAGTCCCTCTCGC	180
Db	41	ThrSerProIlysLeuThrTrrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg	60
Qy	181	CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGCTGAG	240
Db	61	PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu	80
Qy	241	GATCTGGGTGTGTATTACTGTCAACAACCTTGACAGTATCCGCTCACGTCGCTGGTGGT	300
Db	81	AspAlaAlaThrTrrpTyrCysGlnIleArgSerTyrProLeuThrPheGlyAlaGly	100
Qy	301	ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCA	336
Db	101	ThrIlysLeuGluLeuIlysArgAlaAspAlaPro	112

RESULT 2

Q91W12

ID Q91W12 PRELIMINARY; PRT; 235 AA.

AC Q91W12

DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_taxID=10090;

FN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=mix FVB/N;

RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;

RX MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Ioshizuka S., Carinci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=mix FVB/N;

RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;

RA Strausberg R.

RA Submitted (APR-2001) to the EMBL/GenBank/DDJ databases.

DR EMBL; BC006643; AAH06643.1;

DR PDB; 1AY1; X-ray; L-23-232.

DR PDB; 1HQ4; X-ray; A/C-23-235.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig.c1.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig V.

```

KV6F_MOUSE
ID_KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region NQ2-17.4.1.
DE Mus musculus (Mouse)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC 1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; K00735; AAA38680.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Hybridoma; Immunoglobulin V region.
KW FT DOMAIN 1 23 Framework-1.
KW FT DOMAIN 24 33 Complementarity-determining-1.
KW FT DOMAIN 34 48 Framework-2.
KW FT DOMAIN 49 55 Complementarity-determining-2.
KW FT DOMAIN 56 87 Framework-3.
KW FT DOMAIN 88 96 Complementarity-determining-3.
KW FT DOMAIN 97 106 Framework-4.
KW FT DISULFID 23 187 By similarity.

```

FT NON TER 107 107
SQ SEQUENCE 107 AA; 11561 MW; 6P694284ECFA68E6 CRC64;

Alignment Scores:

Pred. No.: 3,83e-38 Length: 107
Score: 421.00 Matches: 82
Percent Similarity: 85.8% Conservative: 9
Best Local Similarity: 77.36% Mismatches: 15
Query Match: 62.46% Indels: 0
DB: 1 Gaps: 0

US-10-049-868A-1 (1-359) x KV6F_MOUSE (1-107)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACCATG 63
Db 2 lilevalLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThrMet 21
QY 64 ACCTGAGTGCAGTCAAGTGTAAATTACATGCACTGTTCCAGCAGGAGTCGGGAC 123
Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTyrTyrGlnGlnLysSerGlyThr 41
QY 124 TTCCCAAAAGAGATTATGACACATCCAACTGGGTTCTGGAGTCCCTGCTCGCTC 183
Db 42 SerProLysArgTrrPileTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 61
QY 184 AGTGCAGTGGTCTGGGACAGAAATTCACCTCGGAAATCAGTAGAGTGAAGGCTCAGGAT 243
Db 62 SerGlySerGlySerAlaThrSerTyrSerLeuThrIleThrSerMetGlnAlaGluAsp 81
QY 244 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGTTCTGGGAC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
QY 304 RAGCTGGAGCTCAACGG 321
Db 102 LysLeuGluLeuLysArg 107

RESULT 6

Q8K1F3 PRELIMINARY; PRT; 112 AA.

AC Q8K1F3;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF516282; AAM64200.1; --
DR PIR; A33933; A33933.
DR PIR; PH1085; PH1085.
DR HSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Alignment Scores:

Pred. No.: 6,48e-38 Length: 112
Score: 419.00 Matches: 81
Percent Similarity: 83.04% Conservative: 12
Best Local Similarity: 72.32% Mismatches: 19
Query Match: 62.17% Indels: 0

DE: 2 Gaps: 0

US-10-049-868A-1 (1-359) x Q8K1F3 (1-112)

QY 1 GACATTGAGTCAACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACC 60
Db 1 AspilevalLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThr 20
QY 61 ATGACCTGAGTGCAGTTCAGTGTAAATTACATGCACTGTTCCAGCAGGAGTCGGGC 120
Db 21 lileSerCysSerAlaSerSerValSerTyrMetTyrTrrPtyrGlnGlnLysProGly 40
QY 121 ACCTTCCCAAAAGAGATTATGACACATCCCAACTGGGTTCTGGAGTCCCTGCTCGC 180
Db 41 SerSerProLysProTrrPileTyrArgThrSerAsnLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGCAGTGGTCTGGGACAGAAATTCACCTCGGAAATCAGTAGAGTGAAGGCTCAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGTTCTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTyrHisSerTyrProTyrThrPheGlyGly 100
QY 301 ACCAAGCTGGAGCTCAACGGGCTGATGCTGCACCA 336
Db 101 ThrLysLeuGluLeuLysArgAlaAspAlaPro 112

RESULT 7

Q8K1F1 PRELIMINARY; PRT; 114 AA.

ID Q8K1F1;
AC Q8K1F1;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF516284; AAM64202.1; --
DR PIR; A33933; A33933.
DR PIR; PH1058; PH1058.
DR HSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3BEFD1 CRC64;

Alignment Scores:

Pred. No.: 6,5e-38 Length: 114
Score: 419.00 Matches: 83
Percent Similarity: 80.70% Conservative: 9
Best Local Similarity: 72.81% Mismatches: 20
Query Match: 62.17% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x Q8K1F1 (1-114)

QY 1 GACATTGAGTCAACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACC 60
Db 1 AspilevalLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThr 20
QY 61 ATGACCTGAGTGCAGTTCAGTGTAAATTACATGCACTGTTCCAGCAGGAGTCGGGC 114


```

Db      21 MetThrCysArgAlaSerSerValSerSerTyrLeuHisTrpTyrGlnGlnLys 40
QY      115 TCGGGCACTTCCCAAAAGAGATTATGACACATCCAAACTGGCTTCTGGAGTCCCT 174
Db      41 SerGlyAlaSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValPro 60
QY      175 GCTGCGCTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAG 234
Db      61 AlaArgPheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGlu 80
QY      235 GCTGAGGATGGGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACCTTCGGT 294
Db      81 AlaGluAspAlaAlaThrTyrTyrCysGlnGlnTyrHisSerTyrProArgThrPheGly 100
QY      295 GCTGGGACCAAGCTGGAGCTGAACGGGCTGATCTGCACCA 336
Db      101 GlyGlyThrLysLeuGluIleLysArgAlaAspAlaAlaPro 114

RESULT 8
KV6I_MOUSE
ID_KV6I_MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region N06-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RL Nature 304:320-324(1983).
CC -I- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
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CC
CC EMBL; K00740; AAA38685.1; -.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
CC Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8B6 CRC64;

Alignment Scores:
Pred. No.: 1,4e-37 Length: 107
Score: 416.00 Matches: 81
Percent Similarity: 84.91% Conservative: 9
Best Local Similarity: 76.42% Mismatches: 16
Query Match: 61.72% Indels: 0

```

```

DB: 1 Gaps: 0
US-10-049-868a-1 (1-359) x KV6I_MOUSE (1-107)
QY 4 ATTGAGCTACCCAGTCTCCAGCAATCATCTCTGCATCTCCAGGGAGAAAGGTCCACATG 63
Db 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThrMet 21
QY 64 ACCTGCAGTCCAGTCAAGTGTATTACATCATCTGGTTCAGCAGGAGTCCGGGACC 123
Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41
QY 124 TTCCCAAAAGAGAGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTC 183
Db 42 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGly***ProAlaArgPhe 61
QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGTGAGGAT 243
Db 62 SerGlySerGlySerAlaThrSerTyrSerLeuThrIleThrSerMetGlnAlaGluAsp 81
QY 244 GTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACCTGCTGGTGGGACC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
QY 304 AAGCTGGAGCTGAACGG 321
Db 102 LysLeuGluLeuLysArg 107

RESULT 9
KV6H_MOUSE
ID_KV6H_MOUSE STANDARD; PRT; 107 AA.
AC P04942;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region N05-61.1.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RL Nature 304:320-324(1983).
CC -I- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
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CC
CC EMBL; K00739; AAA38684.1; -.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
CC Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.

```


Pred. No.: 5,12e-37 Length: 111
 Score: 411.00 Matches: 79
 Percent Similarity: 81.82% Conservative: 11
 Best Local Similarity: 71.82% Mismatches: 20
 Query Match: 60.98% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR10982 (1-111)

QY 10 CTCACCCAGTTCACGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACATGACCTGC 69
 Db 2 MetThrGlnThrProThrIleLeuSerAlaSerProGlyGluValThrMetThrCys 21
 QY 70 AGTGCAGTTCAGGTGTTAATACATGCACCTGCTCCAGCAGGAGTCGGGACCTTCCCC 129
 Db 22 ArgAlaSerSerValSerTyrMetHisTyrGlnGlnLysProGlySerPro 41
 QY 130 AAAAGAGGATTATGACACATCCAACTGGCTCTGGAGTCCCTCGCTCGCTCAGTGGC 189
 Db 42 LysProTyrIleAlaThrSerAsnLeuAlaSerGlyValProAlaArgPheSerGly 61
 QY 190 AGTGGTCTGGACAGAAATCACCTGGAAATCAGTAGTAGTAAGGCTGAGATGGGT 249
 Db 62 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgValGluAlaGluAspAla 81
 QY 250 GTGTATTACTGTCACAACTTGTAGAGTACCGTCACTCGCTGGGCTGGGACCAAGCTG 309
 Db 82 ThrTyrTyrCysGlnGlnTrpSerSerAsnProThrPheGlyGlyThrLysLeu 101
 QY 310 GAGCTGAAACGGCTGTGATGCTGCACCAACT 339
 Db 102 GluIleLysArgAlaAspAlaProThr 111

RESULT 14

ID AAR10994 PRELIMINARY; PRT; 111 AA.

AC AAR10994;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
 DE ANA immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=B6.Sle1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.Sle1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436834; AAR10994.1; --

FT NON_TER 1 111
 SQ SEQUENCE 111 AA; 11914 MW; 69594859D33DA6BF CRC64;

Alignment Scores:
 Pred. No.: 5,12e-37 Length: 111
 Score: 411.00 Matches: 77
 Percent Similarity: 83.64% Conservative: 15
 Best Local Similarity: 70.00% Mismatches: 18
 Query Match: 60.98% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR10994 (1-111)

QY 10 CTCACCCAGTTCACGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACATGACCTGC 69
 Db 2 MetThrGlnThrProAlaIleMetSerAlaSerSerGlyGluValThrMetThrCys 21
 QY 70 AGTGCAGTTCAGGTGTTAATACATGCACCTGCTCCAGCAGGAGTCGGGACCTTCCCC 129
 Db 22 SerAlaSerSerIleSerTyrLeuTyrTyrGlnGlnLysProGlySerPro 41

QY 130 AAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTCGCTCAGTGGC 189
 Db 42 ArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProIleArgPheThrGly 61
 QY 190 AGTGGTCTGGACAGAAATCACCTGGAAATCAGTAGTAGTAAGGCTGAGATGGGT 249
 Db 62 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAla 81
 QY 250 GTGTATTACTGTCACAACTTGTAGAGTACCGTCACTCGCTGGGCTGGGACCAAGCTG 309
 Db 82 ThrTyrTyrCysGlnGlnTrpSerSerTyrProLeuThrValGlyThrGlyThrLysLeu 101
 QY 310 GAGCTGAAACGGCTGTGATGCTGCACCAACT 339
 Db 102 GluLeuLysArgAlaAspAlaProThr 111

RESULT 15

ID AAR11048 PRELIMINARY; PRT; 108 AA.

AC AAR11048;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
 DE ANA immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.Sle1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.Sle1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436888; AAR11048.1; --

FT NON_TER 1 108
 SQ SEQUENCE 108 AA; 11738 MW; C11222F2FDFBC160 CRC64;

Alignment Scores:
 Pred. No.: 6,61e-37 Length: 108
 Score: 410.00 Matches: 77
 Percent Similarity: 84.11% Conservative: 13
 Best Local Similarity: 71.96% Mismatches: 17
 Query Match: 60.83% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR11048 (1-108)

QY 10 CTCACCCAGTTCACGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACATGACCTGC 69
 Db 1 MetThrGlnThrProAlaIleMetSerAlaSerProGlyGluValThrMetThrCys 20
 QY 70 AGTGCAGTTCAGGTGTTAATACATGCACCTGCTCCAGCAGGAGTCGGGACCTTCCCC 129
 Db 21 SerAlaSerSerValSerTyrMetTyrTyrGlnGlnLysProGlySerSerPro 40
 QY 130 AAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTCGCTCAGTGGC 189
 Db 41 ArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProValArgPheSerGly 60
 QY 190 AGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGTAGTCCCTCGCTCAGTGGT 249
 Db 61 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAla 80
 QY 250 GTGTATTACTGTCACAACTTGTAGAGTACCGTCACTCGCTGGGCTGGGACCAAGCTG 309
 Db 81 ThrTyrTyrCysGlnGlnTrpSerSerTyrProTyrThrPheGlyGlyThrLysLeu 100
 QY 310 GAGCTGAAACGGCTGTGATGCT 330
 Db 101 GluIleLysArgAlaAspAla 107

Search completed: October 13, 2004, 13:28:05
Job time : 104.175 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:00:14 ; Search time 82.0429 Seconds
(without alignments)
3139.425 Million cell updates/sec

Title: US-10-049-868A-1

Perfect score: 674

Sequence: 1 gacattgagctcaccagcgc.....gtatccattcgaagcttcc 359

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p.model DBV=xlp
-Q=/cgcn2_1/USPTO.spool_p/US10049868/runat_13102004_132816_24785/app_query.fasta_1.1038
-DB=A_Geneseq_23Sep04 -Qfmt=faстан -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=15
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 @CGN_1_1_308 @runat_13102004_132816_24785 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_23Sep04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471	69.9	215	7 ADE06764	D18 light
2	466	69.1	144	8 ADM79827	Adm79827 Mouse IgG
3	460	68.2	135	2 AAR08347	Aar08347 Light cha
4	459	68.1	129	5 ABB75616	Abb75616 Anti-RANK
5	458	68.0	235	2 AAW41392	Aaw41392 Chimeric
6	452	67.1	108	2 AAR21301	Aar21301 Murine VL
7	452	67.1	156	8 ADO43520	Ado43520 Amino aci
8	451	66.9	215	2 AAR43674	Aar43674 Mouse ant
9	451	66.9	215	2 AAR99644	Aar99644 Anti-bGH
10	451	66.9	215	2 AAR97377	Aar97377 Murine an

11	448	66.5	108	2 AAR21293	Aar21293 Murine VL
12	445	66.0	235	2 AAR13060	Aar13060 Monoclonal
13	444	65.9	241	6 ABR62010	AbR62010 Single-ch
14	444	65.9	255	3 AAB11398	Aab11398 E. coli e
15	444	65.9	255	4 AAB74199	AbB74199 PelB-scfv
16	444	65.9	255	4 AAB70769	AbB70769 Expressio
17	444	65.9	255	4 AAY72020	Aay72020 E. caroto
18	443	65.8	214	2 AAM15933	Aam15933 Antibody
19	443	65.7	118	6 AAE37758	Aae37758 Murine TI
20	443	65.7	118	6 AAE37807	Aae37807 Murine TI
21	441	65.4	316	2 AAY32086	Aay32086 Single ch
22	439	65.1	108	2 AAR21303	Aar21303 Murine VL
23	439	65.1	108	2 AAW41388	Aaw41388 Anti-CEA
24	439	65.1	266	8 ADH77307	Adh77307 Yeast kil
25	439	65.1	309	4 AAB70841	AbB70841 SNV-env 1
26	437	64.8	236	2 AAY34096	Aay34096 Partial a
27	437	64.8	241	2 ABB76197	Abb76197 Anti-meso
28	437	64.8	241	4 AAB50019	AbB50019 Antimesot
29	437	64.8	288	2 AAW82482	Aaw82482 Mouse bis
30	437	64.8	539	3 AAY50823	Aay50823 Fv-antibo
31	437	64.8	554	3 AAY50822	Aay50822 Fv-antibo
32	437	64.8	562	6 ABR57059	AbR57059 Plasmid p
33	436	64.7	109	6 ABU63531	Abu63531 Anti-cucu
34	435	64.5	108	2 AAR21294	Aar21294 Murine VL
35	435	64.5	108	2 AAR21292	Aar21292 Murine VL
36	435	64.5	330	4 AAB70842	AbB70842 SNV-env 1
37	434	64.5	208	2 AAY44175	Aay44175 Mab Fab13
38	433	64.2	108	2 AAR79884	Aar79884 Anti-EGFR
39	433	64.2	108	3 AAB12461	AbB12461 Igg monoc
40	433	64.2	241	5 AAM48925	Aam48925 scfv anti
41	432	64.1	108	3 AAY97236	Aay97236 Variable
42	432	64.1	108	4 AAB82710	AbB82710 VEGF anta
43	432	64.1	108	5 AAE25956	Aae25956 Mouse ant
44	432	64.1	108	5 AAU74413	Aau74413 Antigen-b
45	432	64.1	108	6 ABU26725	AbJ26725 VEGF bind

ALIGNMENTS

RESULT 1
ADE06764
ID ADE06764 standard; protein; 215 AA.

XX ADE06764;

XX 29-JAN-2004 (first entry)

XX D18 light chain protein SEQ ID NO:34.

XX hybrid polypeptide; protein aggregation; prion polypeptide;
XX neuroprotective; nootropic; antidiabetic; anticonvulsant;
XX cerebroprotective; antiparkinsonian; cyostatic; nephrotoxic; cardiant;
XX antiinflammatory; antiarteriosclerotic; gene therapy;
XX Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
XX Alzheimer's disease; Type II diabetes; Huntington's disease;
XX immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
XX ankyrotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
XX Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
XX familial amyloidotic polyneuropathy; medullary carcinoma;
XX chronic renal failure; congestive heart failure; chronic inflammation;
XX atherosclerosis.

OS Synthetic.

XX WO2003085086-A2.

XX 16-OCT-2003.

XX 08-APR-2003; 2003WO-US010856.

XX 09-APR-2002; 2002US-0371610P.

XX (SCRI) SCRIPPS RES INST.

PA

XX Burton DR, Williamson RA, Moroncini G;
XX WPI; 2003-877028/81.
XX N-PSDB; ADE06763.

New motif-grafted hybrid polypeptides binding to the infectious form of a prion, useful for diagnosing or treating diseases of protein aggregation or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or diabetes.

Disclosure: SEQ ID NO 34; 115pp; English.

The present invention describes a hybrid polypeptide (I) comprising: (a) a polypeptide motif containing a sufficient number of contiguous amino acid residues from a polypeptide associated with a disease of protein aggregation or conformation to bind an aggregating form of the polypeptide; and (b) an additional amino acids from a polypeptide other than the polypeptide from which the motif is derived, where the resulting hybrid polypeptide binds with greater affinity to a disease causing or infectious conformer of the polypeptide than is the source of the polypeptide motif compared to a benign form of the polypeptide. Also described: (1) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid molecule; (3) a cell comprising the vector; (4) detecting an isoform or a prpsc form of a prion polypeptide or a polypeptide associated with a disease of protein aggregation, in a sample; (5) a solid support comprising a plurality of polypeptides described above; (6) detecting cells that contain a protein conformer associated with a disease of protein aggregation; (7) preparing a hybrid molecule that specifically interacts with one conformer of a protein involved in the disease mentioned above; and (8) an anti-idiotypic antibody that specifically binds to an infectious form of a prion protein. (I) has neuroprotective, neurotropic, antidiabetic, anticonvulsant, cerebroprotective, antiparkinsonian, cytostatic, nephroprotective, cardiatic, antiinflammatory and antiarteriosclerotic activities, and can be used in gene therapy. The composition and methods of the present invention can be used in diagnosing or treating diseases of protein aggregation or conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine spongiform encephalopathy, Alzheimer's disease, Type II diabetes, Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis associated with chronic inflammatory disease, hereditary systemic amyloidosis associated with autosomal dominant inheritance of variant transthyretin gene, amyotrophic lateral sclerosis, Pick's disease, Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma cell dyscrasias, familial amyloidotic neuropathy, medullary carcinoma of thyroid, chronic renal failure, congestive heart failure, senile cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis or familial amyloidosis. The present sequence is used in the exemplification of the present invention.

Sequence 215 AA;

Alignment Scores:
Pred. No.: 4.15e-41 Length: 215
Score: 471.00 Matches: 91
Percent Similarity: 85.47% Conservative: 9
Best Local Similarity: 77.78% Mismatches: 17
Query Match: 69.88% Indels: 0
DB: 7 Gaps: 0

US-10-049-868A-1 (1-359) x ADE06764 (1-215)

QY 1 GACATTGAGTCCAGCTTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACC 60
Db 3 GlnLeuValLeuThrGlnSerProAlaPheMetSerAlaSerProGlyGlnLysValThr 22
QY 61 ATGACCTGAGTCCAGTTCAGTTGTTAATTACATGCTGGTTCACAGAGAGTCGGGC 120
Db 23 MetThrCysSerAlaSerSerValAsnTyrMetHisTyrTyrGlnGlnLysSerGly 42
QY 121 ACCTTCCCAGAGAGATTATGACATCCAACTGGCTCTGGAGTCCCTGCTCGC 180

Db 43 ThrSerProLysArgTrrPileTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 62
QY 181 CTCAGTGGCAGTGGTCTGGGACACAGATTCCCTCGGAATCAGTAGAGTGAAGCTGAG 240
Db 63 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerMetGluAlaGlu 82
QY 241 GATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACCTTCGGTCTCGG 300
Db 83 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProTyrThrPheGlyGlyGly 102
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTCCACAACTGATCATCTTC 351
Db 103 ThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePhe 119
RESULT 2
ADM79827
ID ADM79827 standard; protein; 144 AA.
XX
AC ADM79827;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mouse IgG2b light chain protein SEQ ID NO:4.
XX
KW cell death-inducing agent; human leukocyte antigen; HLA; antibody;
KW 2D7 antibody; 2D7 antibody degradation product;
KW cell proliferation inhibition; antitumor; autoimmune disease;
KW cytostatic; immunosuppressive; antiinflammatory; dermatological; cancer;
KW Crohn's disease; systemic lupus erythematosus; mouse; IgG2b light chain.
OS Mus musculus.
FN WO2004033499-A1.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-JP013063.
XX
PR 11-OCT-2002; 2002JP-00299289.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
PA (OZAK/) OZAKI S.
PA (ABEM/) ABE M.
PI Ozaki S, Abe M, Tsuchiya M, Kimura N, Kawai S;
XX WPI; 2004-330447/30.
DR N-PSDB; ADM79826.
XX
PT Cell death-inducing agents containing degradation product of antibody particularly diabody recognizing human leukocyte antigen (HLA), applicable in antitumor agents and remedies for autoimmune diseases for treating e.g. cancer.
XX
PS Claim 6; SEQ ID NO 4; 106pp; Japanese.
XX
CC The present invention describes cell death-inducing agents containing the degradation product of an antibody which can recognise human leukocyte antigen (HLA). Also described: (1) a degradation product of the 2D7 antibody; (2) a similar degradation product of an antibody which is: (a) one containing an amino acid sequence of (SEQ ID NO:6) with 253 amino acids; (b) one based on the sequence of (SEQ ID NO:6) but with some amino acids substituted, deleted, inserted and/or added and being functionally equivalent to the parent; (c) one containing the CDR amino-acid sequences of (SEQ ID NO:2) and (SEQ ID NO:4) with 148 and 144 amino acids respectively; or (d) one based on the sequence of (SEQ ID NO:2) and (SEQ ID NO:4) but with some amino acids substituted, deleted, inserted and/or added and being functionally equivalent to the parent; (3) a process for producing an antibody with an increase of activity by degrading a HLA-recognising antibody, or by degrading 2D7 antibody; (4) cell death-inducing agents containing the degradation products of antibody, comprising the produced antibodies or 2D7 antibody as active ingredient; (5) agents for inhibiting cell proliferation containing the degradation

CC products of antibody, comprising the produced antibodies or 2D7 antibody;
 CC (6) antitumour agents containing the degradation products of antibody,
 CC comprising the produced antibodies or 2D7 antibody; and (7) remedies for
 CC autoimmune diseases containing the degradation products of antibody,
 CC comprising the produced antibodies or 2D7 antibody. The 2D7 antibody has
 CC cytosolic, immunosuppressive, antiinflammatory and dermatological
 CC activities. The cell death-inducing agents are applicable in antitumour
 CC agents and remedies for autoimmune diseases for treating e.g. cancer,
 CC Crohn's disease and systemic lupus erythematosus. The present sequence
 CC represents a mouse IgG2b light chain, which is used in the
 CC exemplification of the present invention.

XX
 XX Sequence 144 AA;

Alignment Scores:
 Pred. No.: 1.32e-40 Length: 144
 Score: 466.00 Matches: 90
 Percent Similarity: 85.34% Conservative: 9
 Best Local Similarity: 77.59% Mismatches: 17
 Query Match: 69.14% Indels: 0
 DB: 8 Gaps: 0

US-10-049-868A-1 (1-359) x ADM79827 (1-144)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
 DB 24 IlevalluThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIle 43
 QY 64 ACTGCGAGTCCGAGTTCAGTGTAAATACATGCACCTGGTTCACGAGGAGTCGGGCACC 123
 DB 44 ThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThr 63
 QY 124 TCCCCAAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCTC 183
 DB 64 PheProLysLeuTrpIleTyrSerTyrSerAsnLeuAlaSerGlyValProThrArgPhe 83
 QY 184 AGTGGCAGTGGGTCTGGGACAGCAATTCACCTCGAAATCAGTAGAGTGAAGGCTGAGGAT 243
 DB 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAsp 103
 QY 244 GTGGGTGTATTACTCTCAACACTTGTAGATATCCGCTCAGTTCGGTTCGGTGACCC 303
 DB 104 AlaAlaThrTyrTyrCysGlnGlnArgThrSerTyrProProThrPheGlySerGlyThr 123
 QY 304 AAGCTGGAGCTGAACCGGCTGATGCTGCACCACTGATCCATCTTC 351
 DB 124 LysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePhe 139

RESULT 3
 AAR08347

XX AAR08347 standard; protein; 135 AA.

AC AAR08347;

XX 25-MAR-2003 (revised)

DT 05-MAR-1991 (first entry)

XX Light chain variable region of the BMA-031 Mab.

XX Human alpha/beta T-cell receptor; TCR; cancer; autoimmune disease.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal peptide
 FT Active-site 46..55
 FT /label= CDR 1
 FT Active-site 71..77
 FT /label= CDR 2
 FT Active-site 110..118
 FT /label= CDR 3
 XX

PN EP403156-A.
 XX 19-DEC-1990.
 XX 07-JUN-1990; 90EP-00306178.
 XX 07-JUN-1989; 89US-00362549.
 PR 25-MAY-1990; 90US-00529979.
 XX (GENZ) GENZYME CORP.
 PA (BEHW) BEHRINGER AG.
 XX Kurrie R, Shearman CW, Moore GP, Seiler F;
 XX WPI; 1990-377880/51.
 DR N-PSDB; AAQ06956, AAQ06958.

XX Anti-human alpha-beta T-cell receptor monoclonal antibodies - used for
 PT immunosuppressive therapy in transplantation and as therapeutic agent for
 PT immuno-regulation, e.g. to treat cancer.
 XX Disclosure; Table 1B; 44pp; English.

XX The Mab recognises the epitope on alpha/beta TCR and includes a mediator
 CC response. It is highly effective in clinical application before, after and
 CC during bone marrow transplant surgery, in treatment of cancer and
 CC autoimmune diseases, and has applications in immunoregulation. Abs may
 CC also be used in detection of immunocompetent T-cells. (Updated on 25-MAR-
 CC 2003 to correct PA field.)

XX Sequence 135 AA;

Alignment Scores:
 Pred. No.: 5.64e-40 Length: 135
 Score: 460.00 Matches: 90
 Percent Similarity: 87.50% Conservative: 8
 Best Local Similarity: 80.36% Mismatches: 14
 Query Match: 68.25% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR08347 (1-135)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
 DB 24 IlevalluThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
 QY 64 ACTGCGAGTCCGAGTTCAGTGTAAATACATGCACCTGGTTCACGAGGAGTCGGGCACC 123
 DB 44 ThrCysSerAlaThrSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 63
 QY 124 TCCCCAAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCTC 183
 DB 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 83
 QY 184 AGTGGCAGTGGGTCTGGGACAGCAATTCACCTCGAAATCAGTAGAGTGAAGGCTGAGGAT 243
 DB 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 103
 QY 244 GTGGGTGTATTACTCTCAACACTTGTAGATATCCGCTCAGTTCGGTTCGGTGACCC 303
 DB 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 123
 QY 304 AAGCTGGAGCTGAACCGGCTGATGCTGCACCACT 339
 DB 124 LysLeuGluLeuLysArgAlaAspAlaAlaProThr 135

RESULT 4

ABB75616

ID ABB75616 standard; protein; 129 AA.

XX ABB75616;

XX 10-JUN-2002 (first entry)

XX Anti-RANK ligand mAb 19H22 light chain variable region.

KW RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;
 KW complementarity determining region; CDR; rheumatoid arthritis;
 KW osteoporosis; bone cancer; metastasis; osteolysis; osteoarthritis;
 KW psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;
 KW cytostatic; antiarthritic; antiinflammatory; osteopathic; antidiabetic;
 KW anirheumatic; immunosuppressive; antipsoriatic; neuroprotective;
 KW light chain; VL; mouse.

XX OS Mus musculus.

XX Key Location/Qualifiers

FT Region 24..33
 /label= CDR1
 /note= "complementarity determining region 1"

FT Region 49..55
 /label= CDR2
 /note= "complementarity determining region 2"

FT Region 88..96
 /label= CDR3
 /note= "complementarity determining region 3"

XX WO200215846-A2.

PD 28-FEB-2002.

XX 21-AUG-2001; 2001WO-US026161.

XX 21-AUG-2000; 2000US-0226524P.

PR 07-SEP-2000; 2000US-0230639P.

XX (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

XX Sweet RW, Tornetta MA, Truneh A, Wattam TA;
 WPI; 2002-242022/29.
 N-PSDB; ABL53530.

XX A mouse monoclonal antibody 19H22 for treating or preventing osteopenic
 disease including rheumatoid arthritis and osteoporosis.

PS Claim 6; Page 7; 45pp; English.

XX The present sequence is that of the light chain variable region of
 CC claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)
 CC 19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells
 CC obtained by immunising C56 f1 mice with human RANK-L protein, and fusing
 CC spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for
 CC human RANK-L, having a binding affinity characterised by a dissociation
 CC constant of about 10 power -10 M. RANK-L is a member of the tumour
 CC necrosis factor family of proteins and a key regulator of the immune
 CC system, bone development and homeostasis. The invention provides altered,
 CC chimeric and humanised 19H22 antibodies, including Fab or F(ab')2
 CC fragments, antibodies comprising the light and heavy chain variable
 CC regions of 19H22, and antibodies comprising the complementarity
 CC determining regions of 19H22. These are used in methods for the
 CC diagnosis, treatment and prevention of osteopenic diseases, including
 CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,
 CC wear debris induced osteolysis or osteoarthritis, and immune diseases
 CC including psoriasis, insulin dependent diabetes, inflammatory bowel
 CC disease or multiple sclerosis. Methods are also provided for the
 CC recombinant production of the antibodies, using isolated nucleic acids
 CC and transfected host (preferably mammalian) host cells, and a method of
 CC diagnosing conditions associated with Th1 T-cell activity or osteoclast
 CC development and activation, in particular those listed above

XX Sequence 129 AA;

Alignment Scores: 7.15e-40 Length: 129
 Pred. No.:

Score: 459.00 Matches: 89
 Percent Similarity: 86.21% Conservative: 11
 Best Local Similarity: 76.72% Mismatches: 16
 Query Match: 68.10% Indels: 0
 DB: 5 Gaps: 0

US-10-049-868A-1 (1-359) x ABB/5616 (1-129)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGTCCACCATG 63
 Db 2 IIVallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21

QY 64 ACCTGCAGTCCAGTCAAGTGTAAATTACATGCACCTGTTCCAGCAGAGTCCGGCACC 123
 Db 22 ThrCysSerAlaSerSerValSerTyrMetTyrTrpTyrGlnLysProGlySer 41

QY 124 TTCCTCCAAAAGAGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTGCTC 183
 Db 42 SerProArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProValArgPhe 61

QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTCGGAATCAGTAGAGTGAAGGCTGAGGAT 243
 Db 62 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAsp 81

QY 244 GTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCTGGTCTGGGACC 303
 Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerAsnPheProLeuThrPheGlyAlaGlyThr 101

QY 304 AAGCTGGAGCTGAACGGGCTGATGCTGCACCACTGATCATCATCTTC 351
 Db 102 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 117

RESULT 5
 AAW41392
 ID AAW41392 standard; protein; 235 AA.
 AC AAW41392;
 XX
 XX 17-OCT-2003 (revised)
 DT 02-JUN-1998 (first entry)
 XX
 XX Chimeric anti-CEA antibody 806.077 light chain.
 DE Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
 KW cancer diagnosis; complementarity determining region; light chain.
 XX
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX WO9742329-A1.
 XX 13-NOV-1997.
 PD 29-APR-1997; 97WO-GB0011165.
 PF 04-MAY-1996; 96GB-00009405.
 PR 14-FEB-1997; 97GB-00003103.
 XX (ZENE) ZENECA LTD.
 PA Copley CG, Edge MD, Emery SC;
 PI WPI; 1997-558987/51.
 DR N-PSDB; AAV17288.
 XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
 PT and therapy of cancer.
 XX Example 8; Page 100-101; 208pp; English.
 PS This sequence is the light chain variable region of the antibody of the
 CC invention. The antibody is an anti-CEA (carcinoembryonic antigen)

CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
 CC with DNA encoding the antibody, are used to make the antibody or
 CC conjugate. The conjugate is used in a medicament suitable for intravenous
 CC administration. The conjugate can be used for cancer therapy, selectively
 CC killing tumour cells. The antibody can be used for in vivo or in vitro
 CC diagnosis of cancer. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 235 AA;

Alignment Scores:

Pred. No.: 1.01e-39 Length: 235
 Score: 458.00 Matches: 90
 Percent Similarity: 83.76% Conservativity: 8
 Best Local Similarity: 76.92% Mismatches: 19
 Query Match: 67.95% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAW41392 (1-235)

QY 1 GACATTGAGTCAACCCAGTCTCCAGCAATCATGCTCCAGGGGAGAGGTCAAC 60
 DB 23 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 42
 QY 61 ATGACTGCGAGTCCAGTCAAGTGTATATACATGCACTGGTTCACAGGAGTCCGGC 120
 DB 43 IleThrCysSerAlaSerSerValThrTyrMetHisTrpPheGlnGlnLysProGly 62
 QY 121 ACCTTCCCAAGAGAGGATTATGACATATCAATGCTGCTGAGTCCCTGCTCGC 180
 DB 63 ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 82
 QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGCTGAG 240
 DB 83 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 102
 QY 241 GATGTGGGTGTATTACTGTCAACAACTGTAGAGTATCGCTCAGTTCGGTGTGGG 300
 DB 103 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 122
 QY 301 ACCAAGTGGAGTGAACAGGGGTGATGCTGCACCAACTGTATCCATCTTC 351
 DB 123 ThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhe 139

RESULT 6

AAR21301
 ID AAR21301 standard; protein; 108 AA.

XX AAR21301;

XX 21-MAY-1992 (first entry)

XX Murine VL kappa group IV/VI chain p specific for phox.

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package.
 XX Synthetic.

XX Key Location/Qualifiers
 FH Binding-site 24..33
 FT /label= CDR1
 FT Binding-site 49..55
 FT /label= CDR2
 FT Binding-site 88..96
 FT /label= CDR3
 FT /note= " D-X-G-X-X motif "

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

XX 10-JUL-1990; 90GB-00015198.
 PR 19-OCT-1990; 90GB-00022845.
 PR 12-NOV-1990; 90GB-00024503.
 PR 06-MAR-1991; 91GB-00004744.
 PR 15-MAY-1991; 91GB-00010549.
 XX
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MED RES COUNCIL.

XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD;
 PI WPI; 1992-056862/07.

XX Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic display
 PT package.

XX Example 22; Fig 24; 209pp; English.

XX The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
 CC Fv library. The library produces a diverse repertoire of antibody
 CC fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using
 CC cDNA generated from mRNA from mice immunised with phox coupled to chicked
 CC serum albumin. The VH and VL kappa sequences were separately amplified by
 CC PCR (AAQ23474-84) and ligated into fdCAr2 (AAQ23463) for expression on
 CC the phage surface as fusions with gene III. The resulting library of
 CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
 CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
 CC ; AAR21286-92). Most clones were VH-B combinations so a further
 CC hierarchical library was prepd. by "crossing" VH-B with the VK
 CC repertoire. The resulting library was screened for hapten binding and 24
 CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were
 CC identified. Nearly all the VK genes were "ox-like"; only f, (from the
 CC original library) and h, p, q, and r (from the hierarchical library) were
 CC VKox1 type genes. Of the 24 hierarchical clones, 2 were of type "p". The
 CC Kd of VH-B/Vk-d for phox-GABA was 10 nM, one of the highest values found.
 CC This suggests that phage bearing scfv fragments having weak affinities
 CC can be selected with antigen, probably due to the avidity of the multiple
 CC antibody heads on the phage. The different combinations could also be
 CC isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
 CC AAR22450, 565-581

XX SQ Sequence 108 AA;

Alignment Scores:

Pred. No.: 3.84e-39 Length: 108
 Score: 452.00 Matches: 88
 Percent Similarity: 88.89% Conservativity: 8
 Best Local Similarity: 81.48% Mismatches: 12
 Query Match: 67.06% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR21301 (1-108)

QY 1 GACATTGAGTCAACCCAGTCTCCAGCAATCATGCTCCAGGGGAGAGGTCAAC 60
 DB 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
 QY 61 ATGACTGCGAGTCCAGTTCAGTGTAAATACATGCTGCTCCAGGAGGAGTCCGGC 120
 DB 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysSerGly 40
 QY 121 ACCTTCCCAAGAGAGGATTTATGACATATCAATGCTGCTTCTGGAGTCCCTGCTCGC 180
 DB 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
 QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAATCAGTAGAGTGAAGGCTGAG 240
 DB 61 PheSerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
 QY 241 GATGTGGGTGTATTACTGTCAACAACTGTAGAGTATCCGCTCAGTTCGGTGTGGG 300

Db 81 AspValAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 301 ACCAAGCTGGAGCTCAACGGGCT 324
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 101 ThrLysLeuGluLeLysArgAla 108
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 7

ADO43520
ID ADO43520 standard; protein; 156 AA.

AC ADO43520;

DT 29-JUL-2004 (first entry)

DE Amino acid sequence of variable light chain of antibody BF11.

XX antibody; lipase; biocatalysis; bioconversion; fragrance; flavour;
KW detergent; light chain; monoclonal antibody BF11.

XX Mus musculus.

OS WO2004039845-A1.

PN 13-MAY-2004.

PD 31-OCT-2002; 2002WO-EP012149.

PF 31-OCT-2002; 2002WO-EP012149.

PR (UVR0-) UNIV ROMA DEGLI STUDI LA SAPIENZA.

PA Frati L, Biffoni M, Rughetti A, Koshkaki HR, Barachini S, Nuti M;

PI Palocci C, Soro S, Cernia E;

XX WPI; 2004-376166/35.

DR N-PSDB; ADO43519.

PT New antibodies and polypeptides that recognize microbial lipases and
PT enhance the hydrolytic activity of the enzyme, useful for e.g.
PT biocatalysis or bioconversion reactions, in biosensor technology or
PT bioremediation.

PS Claim 11; Page 32; 42pp; English.

CC The specification describes antibodies or polypeptides for microbial
CC lipase, which enhance the hydrolytic activity of the enzyme. The
CC polypeptides, antibodies or immunocomplex are useful for biocatalysis or
CC bioconversion reactions (e.g. hydrolysis, interesterification,
CC esterification, alcoholysis, acidolysis or aminolysis); in biosensor
CC technology; in bioremediation; in preparing fragrances or flavours and in
CC chemical modification of alcohols, acids, esters or fats; in cosmetic,
CC pharmaceutical and food industries; in preparing detergents; or in
CC identifying, purifying or measuring microbial lipases. The present
CC sequence represents the variable light chain of monoclonal antibody BF11,
CC which is directed against the Candida rugosa lipase.

XX Sequence 156 AA;

Alignment Scores:

Pred. No.: 4.08e-39 Length: 156
Score: 452.00 Matches: 89
Percent Similarity: 84.62% Conservative: 11
Best Local Similarity: 75.21% Mismatches: 18
Query Match: 67.06% Indels: 0
Dbs: 8 Gaps: 0

US-10-049-868A-1 (1-359) x ADO43520 (1-156)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCAC 60

Db 1 GluLeuValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 61 ATGACCTGCAGTCCAGTCAAGTGTTAATTACATGCAGTCTGTTCCACGAGAGTCGGGC 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 21 MetThrCysSerAlaSerSerValArgTyrIleHisTrpTyrGlnGlnLysSerGly 40
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 121 ACCTTCCCCAAAAGAGATTATGACATCCAAACTGGCTTCTGGAGTCCCTGCTCCG 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 41 ThrSerProLysArgTrpIleTyrValThrSerLysArgAlaSerGlyValProAlaArg 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTCAG 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 241 GATGTGGGTGTATTACTGTCAACAACTTTAGAGTATCCGCTCACCTTCGGTCTCGGG 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGly 100
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCATCTTC 351
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 101 ThrLysLeuGluLeLysArgAlaAspAlaAlaProThrValSerIlePhe 117
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 8

AAR43674
ID AAR43674 standard; protein; 215 AA.

AC AAR43674;

DT 25-MAR-2003 (revised)

DT 23-MAY-1994 (first entry)

DE Mouse anti-bovine growth hormone MAB light chain.

XX Monoclonal antibody; Mab; affinity; binding; antigen; diagnostics;
KW therapy; imaging; purification; biosensors.

XX Mus musculus.

XX US5260203-A.

PD 09-NOV-1993.

XX 25-APR-1990; 90US-00512910.

PR 02-SEP-1986; 86US-00902971.

PR 02-SEP-1987; 87US-00092110.

PR 19-JAN-1989; 89US-00299617.

XX (ENZO-) ENZON LABS INC.

PA Ladner RC, Bird RE, Hardman K;

XX WPI; 1993-367875/46.

XX N-PSDB; AAQ51535.

PT Single chain poly:peptide for binding antigen - comprising light and
PT heavy chain antigen binding portions linked by peptide linker.

XX Disclosure; Fig 22; 78pp; English.

XX This sequence is the mature light chain of a monoclonal antibody (MAB)
CC and is the starting material for the production of a single chain
CC polypeptide having binding affinity for a given antigen (Bovine growth
CC hormone). The polypeptide comprises a first polypeptide comprising the
CC antigen binding portion of the light chain variable region of an
CC antibody and a second polypeptide comprising the antigen binding portion
CC of the heavy chain variable region of an antibody and at least one
CC peptide linker linking the first and second polypeptide chains. The
CC resulting single chain polypeptide can be used in diagnostics, therapy
CC (in vivo and in vitro), imaging, purifications and biosensors. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PA field.)

XX Sequence 215 AA;

Alignment Scores:
 Pred. No.: 5,49e-39 Length: 215
 Score: 451.00 Matches: 91
 Percent Similarity: 83.62% Conservative: 6
 Best Local Similarity: 78.45% Mismatches: 17
 Query Match: 66.91% Indels: 2
 DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x AAR93674 (1-215)

QY 10 CTACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACATGACCTGC 69
 |||||
 Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23
 |||||
 QY 70 AGTGCAGGTTCAAGTGT-----AATTACATGCATCTCCAGCAGGAGTCCGGGACC 123
 |||||
 Db 24 ArgAlaSerSerValSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43
 |||||
 QY 124 TTCCCAAAAGAGGATTATGACACATCCAAACTGCTTCTGGAGTCCCTGCTCGCCTC 183
 |||||
 Db 44 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63
 |||||
 QY 184 AGTGCAGGTTCTGGGACAGAAATTCACCTGGAATCATGAGTGAAGGCTGAGGAT 243
 |||||
 Db 64 SerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83
 |||||
 QY 244 GTGGGTGTGTTACTGTCAACACTGTAGAGTATCCGCTCAGTTCCGTTCTGGGACC 303
 |||||
 Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103
 |||||
 QY 304 AAGCTGAGCTGAACCGGCTGATGCTGCACCAACTGTATCCATCTTC 351
 |||||
 Db 104 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 119
 |||||

RESULT 9

AAR93644
 ID AAR93644 standard; protein; 215 AA.

XX AC AAR93644;

XX 25-MAR-2003 (revised)

DT 11-OCT-1996 (first entry)

XX Anti-BGH monoclonal antibody light chain.

XX Antibody engineering; single polypeptide chain binding molecule;
 KW heavy chain; light chain; monoclonal antibody; MAb;
 KW bovine growth hormone; BGH; immunoaffinity purification.

XX Mus sp.

OS US5534621-A.

PN 09-JUL-1996.

PD 06-JUN-1995; 95US-00468992.

PF 02-SEP-1986; 86US-00902971.

PR 02-SEP-1987; 87US-00092110.

PR 19-JAN-1989; 89US-00299617.

PR 25-APR-1990; 90US-00512910.

PR 01-APR-1993; 93US-00040440.

XX (ENZO-) ENZON LABS INC.

XX Bird RE, Ladner RC, Hardman K;

XX WPI; 1996-333309/33.

XX N-PSDB; AAT13734.

XX Immuno:purificn. using single binding chain molecule including antigen-

PT binding parts of antibody light and heavy chain variable regions

PT connected by a linker - is smaller, stabler and less expensive than

complete antibodies.

XX Example; Fig 22; 78pp; English.

CC The mature heavy chain (AAR99643) and mature light chain (AAR99644) of
 CC the mouse anti-bovine growth hormone monoclonal antibody 3C2 can be
 CC utilised in novel single chain binding molecules (AAR99645-48), in which
 CC the hypervariable regions from IgG1 3C2 MAb are joined by peptide linkers
 CC derived from the Fv regions of an IgA class anti-phosphorylcholine
 CC myeloma antibody, MCP-603. The single chain molecules retain the binding
 CC specificity of the light and heavy chains and have the advantages of
 CC smaller size, greater stability and reduced cost. They can be used in
 CC therapy, diagnostics, imaging, purification and biosensors. (Updated on
 CC 25-MAR-2003 to correct PF field.)

XX Sequence 215 AA;

Alignment Scores:

Pred. No.: 5,49e-39 Length: 215
 Score: 451.00 Matches: 91
 Percent Similarity: 83.62% Conservative: 6
 Best Local Similarity: 78.45% Mismatches: 17
 Query Match: 66.91% Indels: 2
 DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x AAR99644 (1-215)

QY 10 CTACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACATGACCTGC 69
 |||||
 Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23
 |||||
 QY 70 AGTGCAGGTTCAAGTGT-----AATTACATGCATCTCCAGCAGGAGTCCGGGACC 123
 |||||
 Db 24 ArgAlaSerSerValSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43
 |||||
 QY 124 TTCCCAAAAGAGGATTATGACACATCCAAACTGCTTCTGGAGTCCCTGCTCGCCTC 183
 |||||
 Db 44 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63
 |||||
 QY 184 AGTGCAGGTTCTGGGACAGAAATTCACCTGGAATCATGAGTGAAGGCTGAGGAT 243
 |||||
 Db 64 SerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83
 |||||
 QY 244 GTGGGTGTGTTACTGTCAACACTGTAGAGTATCCGCTCAGTTCCGTTCTGGGACC 303
 |||||
 Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103
 |||||
 QY 304 AAGCTGAGCTGAACCGGCTGATGCTGCACCAACTGTATCCATCTTC 351
 |||||
 Db 104 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 119
 |||||

RESULT 10

AAR93777

ID AAR93777 standard; protein; 215 AA.

XX AC AAR93777;

XX 25-MAR-2003 (revised)

DT 13-NOV-1996 (first entry)

XX Murine anti-BGH MAb light chain.

XX Antibody engineering; monoclonal antibody; MAb; light chain;
 KW single chain antibody; immunoassay; bovine growth hormone; BGH.

OS Mus musculus.

PN US5518889-A.

XX 21-MAY-1996.

PD 06-JUN-1995; 95US-00468998.

```

PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
PR 25-APR-1990; 90US-00512910.
PR 01-APR-1993; 93US-00040440.
XX (ENZO-) ENZON LABS INC.
XX
XX Bird RE, Ladner RC, Hardman K;
XX
XX WPI; 1996-259060/26.
XX N-PSDB; AAT29057.
XX
XX Immunoassay using single chain antigen binding mol. - as replacement for
XX labelled or immobilised antibody, are less immunogenic, easier to
XX engineer, more stable and less expensive.
XX
XX Example 1; Fig 22; 78pp; English.
XX
XX Portions of the heavy chain (AAR97376) and light chain (AAR97377) of
XX murine IgG1 anti-bovine growth hormone monoclonal antibody 3C2 can be
XX incorporated into novel single polypeptide chain binding molecules (see
XX also AAW02188-90). These are expressed in host cells using DNA constructs
XX (see also AAT36460-62) that include heavy and light chain encoding
XX sequences (AAT29056 and AAT29057) joined by linker moieties. Following
XX expression and refolding, the single chain binding molecules show the
XX binding characteristics of the aggregate of the 2 original heavy and
XX light chains of the variable region of the antibody. (Updated on 25-MAR-
XX 2003 to correct PF field.)
XX
XX Sequence 215 AA;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 5,498-39 Length: 215
XX Score: 451.00 Matches: 91
XX Percent Similarity: 83.62% Conservativity: 6
XX Best Local Similarity: 78.45% Mismatches: 17
XX Query Match: 66.91% Indels: 2
XX DB: 2 Gaps: 1
XX
XX US-10-049-868A-1 (1-359) x AAR97377 (1-215)
QY 10 CTCACCCAGTCTCCAGCAATCATGTCGATCTCCAGGGGAGAGGTCCACCATGACCTGC 69
Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23
QY 70 AGTGCCAGTTCAGTGT-----AATACATGCACTGTTCCACAGAGTCGGGACC 123
Db 24 ArgAlaSerSerSerValSerSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43
QY 124 TTCGCCAAAGAGGATTATGACACATCCAACTGGCTTCGGAGTCCCTGCTCGCCTC 183
Db 44 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63
QY 184 AGTGCCAGTGGTCTGGGACAGAAATTCACCTCGAAATCAGPAGAGTGAAGCTCAGGAT 243
Db 64 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83
QY 244 GTGGGTGTGTATTACTGTCAACAACTGTAGAGTATCGCTACGCTCGCTGCTGGACC 303
Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103
QY 304 AAGCTGGAGCTGAACGGGCTGATGTCGACCAACTGTATCATCTTC 351
Db 104 LysLeuGluLeuLysArgAlaAspAlaProThrValSerIlePhe 119
XX
XX RESULT 11
XX AAR21293
XX ID AAR21293 standard; protein; 108 AA.
XX AC AAR21293;
XX XX
XX DT 21-MAY-1992 (first entry)
XX
XX Murine VL kappa group IV/VI chain h specific for phOx.
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
XX g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Binding-site 24..33 /label= CDR1
XX Binding-site 49..55 /label= CDR2
XX Binding-site 88..96 /label= CDR3
XX /note= " D-X-G-X-X motif "
XX
XX WO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1990; 90GB-00015198.
XX
XX 10-JUL-1990; 90GB-00015198.
XX 19-OCT-1990; 90GB-00022845.
XX 12-NOV-1990; 90GB-00024503.
XX 06-MAR-1991; 91GB-00004744.
XX 15-MAY-1991; 91GB-00010549.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD;
XX WPI; 1992-056862/07.
XX
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic display
XX package.
XX
XX Example 22; Fig 24; 209pp; English.
XX
XX The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
XX Fv library. The library produces a diverse repertoire of antibody
XX fragments specific for 2-phenyl-5-oxazoline (phOx). It was prepd. using
XX cDNA generated from mRNA from mice immunised with phOx coupled to chicked
XX serum albumin. The VH and VL kappa sequences were separately amplified by
XX PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
XX the phage surface as fusions with gene III. The resulting library of
XX clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
XX ; AAR21286-92). Most clones were VH-B combinations so a further
XX hierarchical library was prepd. by "crossing" VH-B with the VK
XX repertoire. The resulting library was screened for hapten binding and 24
XX clones sequenced. 14 new partners (AAR21293-308) for VH-B were
XX identified. Nearly all the VK genes were "ox-like"; only f. (from the
XX original library) and h, p, g, and r (from the hierarchical library) were
XX vkoi type genes. Of the 24 hierarchical clones, 4 were of type "h". The
XX kd of VH-B/VK-d for phOx-GABA was 10 nM, one of the highest values found.
XX This suggests that phage bearing scFv fragments having weak affinities
XX can be selected with antigen, probably due to the avidity of the multiple
XX antibody heads on the phage. The different combinations could also be
XX isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
XX AAR22450, 565-581
XX
XX Sequence 108 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1,02e-38 Length: 108
XX Score: 448.00 Matches: 87
XX Percent Similarity: 87.96% Conservativity: 8
XX

```

Best Local Similarity: 80.56% Mismatches: 13
 Query Match: 66.47% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR21293 (1-108)

QY 1 GACATTGAGCTACCCAGTCTCCAGCAATCATGTCATCTCCAGGGGAGAGGTCAACC 60
 DB 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY 61 ATGACCTGCAGTCCAGTTCAGGTGTTAATACATGCACTGCTCCAGCAGGAGTCCGGC 120
 DB 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY 121 ACCTTCCCAAAAGAGGATTATGACACATCCAACTGGCTCTGGAGTCCCTGCTCGC 180
 DB 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY 181 CTCAGTGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAG 240
 DB 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY 241 GATGTGGGTGCTATTACTGTCACAACTTGTAGATATCCGCTCAGCTTCGGTGGTGGG 300
 DB 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100

QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
 DB 101 ThrLysLeuGluIleLysArgAla 108

RESULT 12
 AAR13060
 ID AAR13060 standard; protein; 235 AA.
 AC AAR13060;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-OCT-1991 (first entry)
 XX
 DE Monoclonal antibody OK3T light chain.
 XX
 KW OK3T; light chain; humanised antibodies; CDR-grafting.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /label= signal peptide
 FT 23..235
 FT /label= light chain
 XX
 PN WO9109967-A.
 XX
 PD 11-JUL-1991.
 XX
 PF 21-DEC-1989; 89GB-00028874.
 XX
 PR 21-DEC-1989; 89GB-00028874.
 PR 21-DEC-1990; 90WO-GB002017.
 XX
 PA (CLLT) CELITECH LTD.
 XX
 PI Adair JR, Athwal DS, Emtage JS;
 XX
 DR WPI; 1991-222915/30.
 DR P-PSDB; AAR13060.
 XX
 XX New humanised antibodies comprising CDR grafted antibody - with heavy and
 PT light chains, for use in vivo therapy and diagnosis.
 PT
 PS Disclosure; Fig 1b; 91pp; English.
 XX
 CC The OK3T light chain sequence was deduced from the cDNA sequence isolated

CC from a library prepared from OK3T producing cells. The library was
 CC screened with a probe complementary to a region in the mouse kappa
 CC constant region. The OK3T sequence was used in CDR-grafting experiments
 CC to prepare humanised antibodies. NOTE: Data found in patent WO9109968 has
 CC been used to index this entry. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 SQ Sequence 235 AA;
 Alignment Scores:
 Pred. No.: 2,41e-38 Length: 235
 Score: 445.00 Matches: 87
 Percent Similarity: 83.62% Conservative: 10
 Best Local Similarity: 75.00% Mismatches: 19
 Query Match: 66.02% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR13060 (1-235)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCATCTCCAGGGGAGAGGTCAACATG 63
 DB 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43

QY 64 ACCTGSCAGTCCAGTTCAGGTGTTAATTACATGCACTGGTTCACGAGGAGTCCGGCACC 123
 DB 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63

QY 124 TTCCCAAAAGAGGATTATGACACATCCAACTGGCTCTGGAGTCCCTGCTCGGCTC 183
 DB 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83

QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGAT 243
 DB 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103

QY 244 GTGGGTGTATTACTGTCAACAACTGTAGAGTATCCGCTCAGTTCGGTGGGACC 303
 DB 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123

QY 304 AAGCTGGAGCTGAACCGGCTGATGTCGACCAACTGTATCCATCTTC 351
 DB 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 13
 ABR62010
 ID ABR62010 standard; protein; 241 AA.
 XX
 AC ABR62010;
 XX
 DT 03-OCT-2003 (first entry)
 XX
 DE Single-chain (scFv) antibody.
 XX
 KW Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy;
 KW antisense therapy; scFv; antibody.
 XX
 OS Synthetic.
 XX
 PN EP1321524-A1.
 XX
 PD 25-JUN-2003.
 XX
 PF 19-DEC-2001; 2001EP-00130319.
 XX
 PR 19-DEC-2001; 2001EP-00130319.
 XX
 PA (DUEP/) DUERING K.
 XX
 PI Mahn A, Hantke S, Petsch D;
 XX
 DR WPI; 2003-543829/52.
 DR N-PSDB; ACC84876.
 XX

PT Increasing the content of transgene-coded biomolecules in a plant or
 PT animal, useful for producing proteins for diagnosing, preventing and/or
 PT treating viral diseases and cancer, comprises changing the distribution
 PT of ATP and/or ADP.

XX Example 2; Fig 2; 18pp; English.

XX The invention relates to increasing the content of one or more transgene-
 CC coded biomolecules in an organism and involves changing the distribution
 CC of ATP and/or ADP in cells of the organism. The yield of transgenic
 CC molecules in host cells is often insufficient for industrial production.
 CC The method increases the yield of transgenic molecules in animal and
 CC plant host cells, therefore facilitating their production on an
 CC industrial scale. The proteins produced by the method are useful for
 CC diagnosing, preventing and/or treating viral diseases and cancer. The
 CC present sequence represents a single-chain (scfv) antibody, used to
 CC exemplify the increase in the expression of scfv antibodies in transgenic
 CC potato tubers

XX Sequence 241 AA;

Alignment Scores:
 Pred. No.: 3,09e-38 Length: 241
 Score: 444.00 Matches: 88
 Percent Similarity: 86.36% Conservative: 7
 Best Local Similarity: 80.00% Mismatches: 15
 Query Match: 65.88% Indels: 0
 DB: 6 Gaps: 0

US-10-049-868A-1 (1-359) x ABR62010 (1-241)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGTCCACC 60
 DB |||||
 QY 61 ATGACCTGCAGTCCAGTTCAGTGTAAATACATGCACCTGTTCCAGCAGGAGTCCGGC 120
 DB |||||
 QY 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnSerGly 171
 QY 121 ACCTTCCCAAGAGGATTTATGACATCATCAACCTGGCTCTGGAGTCCCTGCTCGC 180
 DB |||||
 QY 172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerGlyValProAlaArg 191
 QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGCTGAG 240
 DB |||||
 QY 192 PheSerGlySerGlySerGlyThrSerThrSerLeuThrIleSerSerMetGluAlaGlu 211
 QY 241 GATGTGGTGTGTATTACTGTCAACAATTTAGAGTATCCGCTCACGTTCGGTCTGGG 300
 DB |||||
 QY 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231
 QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
 DB |||||
 QY 232 ThrLysLeuGluLeuLysArgAlaAla 241

RESULT 14

ID AAB11398
 XX AAB11398 standard; protein; 255 AA.

AC AAB11398;

XX AAB11398;

DE 22-FEB-2001 (first entry)

XX E. coli expression plasmid PUBS520-ScFvOx encoded protein.

XX Eukaryotic protein; protease; interferon; antibody; hormone;

XX disulfide bridge.

XX Escherichia coli.

XX Synthetic.

XX EF1048732-A1.

XX

PD 02-NOV-2000.
 XX
 PF 26-APR-1999; 99EP-00107412.
 XX
 PR 26-APR-1999; 99EP-00107412.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX WPI, 2000-674185/66.
 DR N-PSDB; AAC66074.

XX Preparation of water-soluble eukaryotic polypeptides with disulfide
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
 PT presence of arginine or amide compound.

XX Example 6; Page 22-23; 40pp; German.

XX This invention describes a novel preparation of a water-soluble,
 CC naturally occurring eukaryotic polypeptide containing two or more
 CC cysteine units bound via a disulfide bridge which comprises cultivation
 CC of prokaryotic cells in the presence of arginine or an amide compound.
 CC The method is useful for the preparation of eukaryotic proteins e.g.
 CC proteases, interferons, protein hormones, antibodies or antibody
 CC fragments (e.g. a single chain FV fragment that binds to thyroid
 CC stimulating hormone). It is especially useful for preparing proteins with
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator
 CC (rPA). The technique is simple and does not require in vitro after-
 CC treatment, such as the removal of inclusion bodies, reduction or
 CC naturalization

XX Sequence 255 AA;

Alignment Scores:
 Pred. No.: 3,12e-38 Length: 255
 Score: 444.00 Matches: 88
 Percent Similarity: 86.36% Conservative: 7
 Best Local Similarity: 80.00% Mismatches: 15
 Query Match: 65.88% Indels: 0
 DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x AAB11398 (1-255)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGTCCACC 60
 DB |||||
 QY 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151
 QY 61 ATGACCTGCAGTCCAGTTCAGTGTAAATACATGCACCTGTTCCAGCAGGAGTCCGGC 120
 DB |||||
 QY 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnSerGly 171
 QY 121 ACCTTCCCAAGAGGATTTATGACATCATCAACCTGGCTCTGGAGTCCCTGCTCGC 180
 DB |||||
 QY 172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191
 QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGCTGAG 240
 DB |||||
 QY 192 PheSerGlySerGlySerGlyThrSerThrSerLeuThrIleSerSerMetGluAlaGlu 211
 QY 241 GATGTGGTGTGTATTACTGTCAACAATTTAGAGTATCCGCTCACGTTCGGTCTGGG 300
 DB |||||
 QY 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231
 QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
 DB |||||
 QY 232 ThrLysLeuGluLeuLysArgAlaAla 241

RESULT 15

AAB74199
 ID AAB74199 standard; protein; 255 AA.

XX AAB74199;

AC AAB74199;

XX 29-MAY-2001 (first entry)

DT

XX PeIB-scFvOxazolone fusion protein.
XX Molecular chaperone; PelB signal sequence; scFvOxazolone.
XX Unidentified.
XX EP1077262-A1.
XX 21-FEB-2001.
XX 24-JUL-2000; 2000EP-00115839.
XX 29-JUL-1999; 99EP-00114811.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
XX WPI; 2001-246712/26.
XX N-PSDB; AAF77806.

XX Producing naturally folded eukaryotic proteins e.g. antibodies,
XX interferon, hormones or proteases that contain two or several cysteines
XX linked by disulfide bridges comprises co-expression of a molecular
XX chaperone.
XX Disclosure; Page 19; 35pp; English.
XX The present invention relates to a method for production of a naturally
XX folded eukaryotic protein containing two or more cysteines linked by
XX disulfide bridges. The method comprises co-expression and secretion into
XX the periplasm of a molecular chaperone via an expression vector coding
XX for the chaperone. The expression vector also encodes a signal sequence.
XX The method is useful for producing a naturally folded eukaryotic protein
XX such as an antibody, antibody fragment, interferon, protein hormone or a
XX protease containing two or several cysteines linked by disulfide bridges.
XX The present sequence is a fusion protein composed of the PelB signal
XX sequence and scFvOxazolone. This sequence was used in the method of the
XX present invention
XX SQ Sequence 255 AA;

Alignment Scores:
Pred. No.: 3.12e-38 Length: 255
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x AAB74199 (1-255)

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Db |||||
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QY 121 ACCTTCCCAAGAGGATTATGACACATCCAACTGGCTCTCGAGTCCCTGCTCGC 180
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QY 181 CTCAGTGGCGTGGTCTGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGCTGAG 240
Db |||||
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QY 241 GATGTGGGTGTATTACTGTCAACAATCTGTAGAGTATCCGCTCAGCTTCGGTGGTGGG 300
Db |||||
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QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db |||||
232 ThrLysLeuGluLeuLysArgAlaAla 241

Search completed: October 13, 2004, 13:21:04
Job time : 84.0429 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:28:16 ; Search time 69.6122 seconds
(without alignments)
3328.244 Million cell updates/sec

Title: US-10-049-868A-1
Perfect score: 674
Sequence: 1 gacattgagctcaccagctc.....gtatccatcttcaagcttcc 359

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 2713116

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV_TIMEOUT=130 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-410-907A-34
; Sequence 34, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Gianluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Light Chain

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2	459	68.1	129	14	US-10-344-779-2	Sequence 2, Appl
3	459	68.1	129	16	US-10-738-809-2	Sequence 2, Appl
4	458	68.0	235	9	US-09-910-059-17	Sequence 17, Appl
5	452	67.1	108	16	US-10-803-622-251	Sequence 251, App
6	452	67.1	108	16	US-10-803-653-251	Sequence 251, App
7	448	66.5	108	16	US-10-803-622-243	Sequence 243, App
8	448	66.5	108	16	US-10-803-653-243	Sequence 243, App
9	446	66.2	108	16	US-10-803-622-241	Sequence 241, App
10	446	66.2	108	16	US-10-803-653-241	Sequence 241, App
11	445	66.0	235	10	US-09-795-515-5	Sequence 5, Appl
12	445	66.0	235	15	US-10-704-352-5	Sequence 5, Appl
13	445	66.0	235	15	US-10-704-071-5	Sequence 5, Appl
14	440	65.3	107	9	US-09-144-886-82	Sequence 82, Appl
15	440	65.3	107	9	US-09-144-886-83	Sequence 83, Appl
16	439	65.1	108	9	US-09-910-059-9	Sequence 9, Appl
17	439	65.1	108	16	US-10-803-622-253	Sequence 253, App
18	439	65.1	108	16	US-10-803-653-253	Sequence 253, App
19	436	64.7	108	16	US-10-803-622-242	Sequence 242, App
20	436	64.7	108	16	US-10-803-653-242	Sequence 242, App
21	432	64.1	107	16	US-10-632-706-79	Sequence 79, Appl
22	432	64.1	107	16	US-10-632-706-80	Sequence 80, Appl
23	432	64.1	108	9	US-09-976-787-8	Sequence 8, Appl
24	432	64.1	108	9	US-09-865-198-8	Sequence 8, Appl
25	432	64.1	240	9	US-09-976-787-28	Sequence 28, Appl
26	432	64.1	240	9	US-09-865-198-27	Sequence 27, Appl
27	432	64.1	669	9	US-09-807-721-2	Sequence 2, Appl
28	428	63.5	108	16	US-10-803-622-240	Sequence 240, App
29	428	63.5	108	16	US-10-803-653-240	Sequence 240, App
30	427	63.4	108	16	US-10-803-622-252	Sequence 252, App
31	427	63.4	108	16	US-10-803-653-252	Sequence 252, App
32	427	63.4	110	16	US-10-803-622-256	Sequence 256, App
33	427	63.4	110	16	US-10-803-653-256	Sequence 256, App
34	427	63.4	256	14	US-10-247-488-2	Sequence 2, Appl
35	427	63.4	258	14	US-10-247-488-4	Sequence 4, Appl
36	425	63.1	108	16	US-10-803-622-244	Sequence 244, App
37	425	63.1	108	16	US-10-803-653-244	Sequence 244, App
38	424	62.9	110	16	US-10-803-622-255	Sequence 255, App
39	424	62.9	110	16	US-10-803-653-255	Sequence 255, App
40	424	62.9	119	9	US-09-808-037-28	Sequence 28, Appl
41	424	62.9	119	14	US-10-162-889-28	Sequence 28, Appl
42	424	62.9	119	15	US-10-384-788-28	Sequence 28, Appl
43	424	62.9	119	15	US-10-618-856-26	Sequence 26, Appl
44	424	62.9	239	9	US-09-808-037-6	Sequence 6, Appl
45	424	62.9	239	14	US-10-162-889-6	Sequence 6, Appl

Qy 61 ATGACCTGCACTGCAGTTCAGCTGTTAATTAATACATGCACTGGTCCACAGAGTCGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
Qy 121 ACCTTCCCAAAAGAGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
Qy 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
Qy 241 GATGTGGGTGTATTACTGTCAACAACCTTGAGAGTATCCGCTACAGTTCGGTCTGGC 300
Db 81 AspValAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100
Qy 301 ACCAAGCTGGAGCTGAAACGGGCT 324
Db 101 ThrLysLeuGluIleLysArgAla 108

RESULT 6

US-10-803-653-251
; Sequence 251, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 251
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-251

Alignment Scores:

Pred. No.: 4, 3e-38 Length: 108
Score: 452.00 Matches: 88
Percent Similarity: 88.89% Conservative: 8
Best Local Similarity: 81.48% Mismatches: 12
Query Match: 67.06% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-803-653-251 (1-108)

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Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
Qy 61 ATGACCTGCACTGCAGTTCAGCTGTTAATTAATACATGCACTGGTCCACAGAGTCGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
Qy 121 ACCTTCCCAAAAGAGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
Qy 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGCTGAG 240
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RESULT 7

US-10-803-622-243
; Sequence 243, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857

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; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-243

Alignment Scores:
Pred. No.: 1.12e-37 Length: 108
Score: 448.00 Matches: 87
Percent Similarity: 87.96% Conservative: 8
Best Local Similarity: 80.56% Mismatches: 13
Query Match: 66.47% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-803-622-243 (1-108)
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DB 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
QY 121 ACCTTCCCAAGAGAGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
DB 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGGCTGAG 240
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QY 301 ACCAAGCTGGAGCTGAACCGGCT 324
DB 101 ThrLysLeuGluIleLysArgAla 108

RESULT 8
US-10-803-653-243
; Sequence 243, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
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; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-243

Alignment Scores:
Pred. No.: 1.12e-37 Length: 108
Score: 448.00 Matches: 87
Percent Similarity: 87.96% Conservative: 8
Best Local Similarity: 80.56% Mismatches: 13
Query Match: 66.47% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-803-653-243 (1-108)
QY 1 GACATTGAGTCCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
DB 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTCCAGTCAAGTGTAAATACATGACACTGGTTCAGAGGAGTCGGGC 120
DB 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
QY 121 ACCTTCCCAAGAGAGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
DB 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGGCTGAG 240
DB 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGGTGTGTTACTGTCAACACTTGTAGAGTATCCGCTCAGTTCGGTGTGGG 300
DB 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100
QY 301 ACCAAGCTGGAGCTGAACCGGCT 324
DB 101 ThrLysLeuGluIleLysArgAla 108

RESULT 9
US-10-803-622-241
; Sequence 241, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Griffiths, Andrew
```

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: APPLICANT: Jackson, Ronald
: APPLICANT: Holliger, Kasper
: APPLICANT: Marks, James
: APPLICANT: Clackson, Timothy
: APPLICANT: Chiswell, David
: APPLICANT: Winter, Gregory
: APPLICANT: Bonett, Timothy
: TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
: FILE REFERENCE: 13839-00013
: CURRENT APPLICATION NUMBER: US/10/803,622
: CURRENT FILING DATE: 2004-03-18
: PRIOR APPLICATION NUMBER: GB 9015198.6
: PRIOR FILING DATE: 1990-07-10
: PRIOR APPLICATION NUMBER: GB 9022845.3
: PRIOR FILING DATE: 1990-10-19
: PRIOR APPLICATION NUMBER: GB 9022845.3
: PRIOR FILING DATE: 1990-10-19
: PRIOR APPLICATION NUMBER: GB 9024503.6
: PRIOR FILING DATE: 1990-11-12
: PRIOR APPLICATION NUMBER: GB 9104744.9
: PRIOR FILING DATE: 1991-03-06
: PRIOR APPLICATION NUMBER: GB 9110549.4
: PRIOR FILING DATE: 1991-05-15
: PRIOR APPLICATION NUMBER: PCT/GB91/01134
: PRIOR FILING DATE: 1991-07-10
: PRIOR APPLICATION NUMBER: US 07/971,857
: PRIOR FILING DATE: 1993-01-08
: PRIOR APPLICATION NUMBER: US 08/484,893
: PRIOR FILING DATE: 1995-06-07
: NUMBER OF SEQ ID NOS: 272
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 241
: LENGTH: 108
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-241

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Alignment Scores:
Pred. No.:      1.8e-37      Length:      108
Score:          446.00      Matches:     87
Percent Similarity: 87.04%   Conservative: 7
Best Local Similarity: 80.56% Mismatches:    14
Query Match:      66.17%     Indels:      0
DB:               16        Gaps:        0

US-10-049-868A-1 (1-359) x US-10-803-622-241 (1-108)

QY      1  GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCAAC 60
      |||
Db      1  AsplleGluLeuThrGlnSerProAlaIleMetSerAlaIleProGlyGluIysValThr 20

QY     61  ATGACCTTCAGTGCAGGTCGAAGTGTAAATACATGCACCTGGTTCACAGAGAGTCGGGC 120
      |||
Db     21  MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY    121  ACCTTCCCAAAAGAGGATTATGACACATCCAAACTCGGCTTCTCGAGTCCCTGCTGCGC 180
      |||
Db    41  ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaIle 60

QY    181  CTCAGTGGCAGTGGGTCTGGGACAGAAATCACCTCGGAATCAGTAGAGTGAAGGCTGAG 240
      |||
Db    61  PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY   241  GATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCAGGTTCCGCTGCTGGG 300
      |||
Db   81  AspAlaAlaThrTyrTyrCysGlnGlnPheSerSerAsnProIleuThrPheGlyAlaGly 100

QY   301  ACCAAGCTGGAGCTGAACCGGGCT 324
      |||
Db  101  ThrLysLeuGluLeuLysArgAla 108

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; FEATURE:
;   OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-241

```

Alignment Scores:	1.8e-37	Length:	108
Pred. No.:	Score:	Matches:	87
	446.00	Conservative:	7
Percent Similarity:	87.04%	Mismatches:	14
Best Local Similarity:	80.56%	Indels:	0
Query Match:	66.17%	Gaps:	0
DB:	16		

QY 181 CTCAGTGGAGGTCTGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAG 240
 |||||
 Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
 |||||
 QY 241 GATGGGTGTGTATTACTGTCAACAACCTGTGAGAGTATCCGCTCACGTTGGTGGTGGG 300
 |||||
 Db 81 AspAlaAlaThrTyrTyrCysGlnGlnPheSerSerAsnProLeuThrPheGlyAlaGly 100
 |||||
 QY 301 ACCAAGCTGGAGCTCAAAACGGGCT 324
 |||||
 Db 101 ThrLysLeuGluLeuLysArgAla 108
 |||||

RESULT 11

US-09-795-515-5
 ; Sequence 5, Application US/09795515
 ; Publication No. US20030039645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Athwal, Diljeet S.
 ; APPLICANT: Emtage, John S.
 ; TITLE OF INVENTION: Humanised Antibodies
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/846,658
 ; FILING DATE: 01-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Trujillo, Doreen Yatko
 ; REGISTRATION NUMBER: 35,719
 ; REFERENCE/DOCKET NUMBER: CARP-0057
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-795-515-5

Alignment Scores:
 Pred. No.: 2,49e-37 Length: 235
 Score: 445.00 Matches: 87
 Percent Similarity: 83.62% Conservative: 10
 Best Local Similarity: 75.00% Mismatches: 19
 Query Match: 66.02% Indels: 0
 DB: 10 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-795-515-5 (1-235)

QY 4 ATTGAGTCAACCCAGTCTCCAGCAATCATGTCTCATCTCCAGGGAGAGGTCCACCATG 63
 |||||
 Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
 |||||
 QY 64 ACTGCAGTCCCAAGTTCACAGTTAATTACATGCTGTTCACGAGGAGTGGGCACC 123
 |||||

Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTTPyrGlnGlnLysSerGlyThr 63
 QY 124 TTCCCCAAAAGAGATTATGACATCAATCGCTTCTGGAGTCCCTGCTCGCCTC 183
 |||||
 Db 64 SerProLysArgTTPilleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
 |||||
 QY 184 AGTGGCAGTGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
 |||||
 Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
 |||||
 QY 244 GTGGGTGTGTATTACTGTCAACAACCTGTGACAGTATCCGCTCACGTTGGTGGTGGGACC 303
 |||||
 Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
 |||||
 QY 304 AAGCTGGAGTGAACCGGCTGATGCTGCACCAACTGTATCCATCTTC 351
 |||||
 Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139
 |||||

RESULT 12

US-10-704-352-5
 ; Sequence 5, Application US/10704352
 ; Publication No. US20040071693A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Athwal, Diljeet S.
 ; APPLICANT: Emtage, John S.
 ; TITLE OF INVENTION: Humanised Antibodies
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10704,352
 ; FILING DATE: 07-Nov-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/795,515
 ; FILING DATE: 28-FEB-2001
 ; APPLICATION NUMBER: 08/846,658
 ; FILING DATE: 01-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Trujillo, Doreen Yatko
 ; REGISTRATION NUMBER: 35,719
 ; REFERENCE/DOCKET NUMBER: CARP-0057
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-10-704-352-5

Alignment Scores:
 Pred. No.: 2,49e-37 Length: 235
 Score: 445.00 Matches: 87
 Percent Similarity: 83.62% Conservative: 10
 Best Local Similarity: 75.00% Mismatches: 19
 Query Match: 66.02% Indels: 0
 DB: 15 Gaps: 0

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US-10-049-868A-1 (1-359) x US-10-704-352-5 (1-235)
QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGTCCACCATG 63
Db 24 lIeValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCAGTCAAGTGTAAATTACATGCACTGGTTCACGAGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAAGATTATGACACATCCAACTGGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGGTCTCGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTCAACGGGCTGATCTGCACCACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 13
US-10-704-071-5
; Sequence 5, Application US/10704071
; Publication No. US20040076627A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Attwal, Diljeet S.
; Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Nov-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-704-071-5
Alignment Scores:
QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGTCCACCATG 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 20
QY 61 ATGACCTGCAGTGCAGTCAAGTGTAAATTACATGCACTGGTTCACGAGAGTCGGGCACC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

US-10-049-868A-1 (1-359) x US-10-704-071-5 (1-235)
QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGTCCACCATG 63
Db 24 lIeValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCAGTCAAGTGTAAATTACATGCACTGGTTCACGAGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAAGATTATGACACATCCAACTGGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGGTCTCGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTCAACGGGCTGATCTGCACCACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

US-09-144-886-82
; Sequence 82, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1E8 region VL epitope 1
US-09-144-886-82
Alignment Scores:
QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGTCCACCATG 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 20
QY 61 ATGACCTGCAGTGCAGTCAAGTGTAAATTACATGCACTGGTTCACGAGAGTCGGGCACC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:12:25 ; Search time 21.6191 Seconds
(without alignments)
3231.093 Million cell updates/sec

Title: US-10-049-868A-2
Perfect score: 673
Sequence: 1 caggtgcagctgcaggatc.....ccacggtcacggtctctctca 363

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2 1/USPTO spool_P/US10049868/runat_13102004_132817_24805/app_query.fasta_1.1038
-DB=PIR_79 -QPWT=Easton -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US10049868 @CGN 1 1 77 @runat 13102004 132817 24805 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	552.5	82.1	141	2 S52446	Ig heavy chain V r
2	536	79.6	112	2 S11100	Ig heavy chain V r
3	533.5	79.3	117	2 S38563	Ig heavy chain V r
4	530.5	78.8	120	2 PLO087	Ig heavy chain V r
5	529	78.6	140	2 S55028	Ig heavy chain V r
6	527	78.3	113	2 S11101	Ig heavy chain V r
7	527	78.3	114	2 S11106	Ig heavy chain V r
8	527	78.3	116	2 S11102	Ig heavy chain V r
9	524.5	77.9	139	2 A32456	Ig heavy chain pre
10	521	77.4	112	2 S11108	Ig heavy chain V r
11	517	76.8	115	2 S11103	Ig heavy chain V r
12	515	76.5	114	2 S11099	Ig heavy chain V r
13	507.5	75.4	116	2 S42484	Ig heavy chain V r
14	500.5	74.4	122	2 A49049	Ig heavy chain V r

15	500	74.3	106	2 S26322	Ig heavy chain V r
16	499	74.1	118	2 P00266	Ig heavy chain V r
17	497.5	73.9	135	2 S31913	Ig gamma-2A chain
18	492.5	73.2	122	2 S20809	Ig heavy chain V r
19	492	73.1	106	2 S14489	Ig heavy chain V r
20	492	73.1	114	2 S11105	Ig heavy chain V r
21	491	73.0	112	2 S11098	Ig heavy chain V r
22	490	72.8	117	2 S10111	Ig heavy chain V r
23	489	72.7	140	2 S14238	Ig gamma-1 chain p
24	487	72.4	127	2 B31807	Ig heavy chain V r
25	487	72.4	144	1 G2MS14	Ig heavy chain pre
26	486.5	72.3	118	2 S32786	Ig heavy chain (an
27	483	71.8	121	2 D30560	Ig heavy chain V r
28	480	71.3	121	2 S33131	Ig heavy chain V r
29	480	71.3	231	2 PC4155	Ig heavy chain V r
30	479	71.2	109	2 S11109	Ig gamma-2b chain
31	479	71.2	114	2 S11104	Ig heavy chain V r
32	478.5	71.1	144	2 S11244	Ig heavy chain V r
33	477	70.9	107	2 S14492	Ig gamma-2a chain
34	476	70.7	107	2 S14493	Ig heavy chain V r
35	475	70.6	100	2 S14490	Ig heavy chain V r
36	473	70.3	115	2 S11107	Ig heavy chain V r
37	471	70.0	111	2 S26324	Ig heavy chain V r
38	471	70.0	114	2 S26321	Ig heavy chain V r
39	470	69.8	107	2 S14491	Ig heavy chain V r
40	467.5	69.5	110	2 PH1024	Ig heavy chain V r
41	467	69.4	95	2 S17605	Ig heavy chain V r
42	464	68.9	110	2 S26323	Ig heavy chain V r
43	463	68.8	109	2 PH1025	Ig heavy chain V r
44	461.5	68.6	115	2 S26470	Ig heavy chain V r
45	455	67.6	101	2 S03466	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S52446

Ig heavy chain V region precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999

C/Accession: S52446

R/Berdoz, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A/Description: Specific amplification by the polymerase chain reaction of rearranged ge

A/Reference number: S52445

A/Accession: S52446

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-141 <BER>

A/Cross-references: EMBL:X82692; NID:g673441; PIDN:CAA58013.1; PID:g673442

C/Genetics:

A/Introns: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1.06e-46	Length:	141
Score:	552.50	Matches:	109
Percent Similarity:	90.98%	Conservative:	2
Best Local Similarity:	89.34%	Mismatches:	10
Query Match:	82.10%	Indels:	1
DB:	2	Gaps:	1

US-10-049-868A-2 (1-363) x S52446 (1-141)

QY 1 CAGGTGCAGCTCAGAGCTCGACCTGGCGCCCTCAGAGCCTGTCCATC 60

Db 20 GlnValGlnLeuSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39

QY 61 ACTTGCACCTGCTCTGGGATTTTCATTAAACAGATATGGTGCTACCTGGGTTCGCGAGCCT 120

Db 40 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 59

Score: 530.50 Matches: 104
 Percent Similarity: 88.43% Conservative: 3
 Best Local Similarity: 85.95% Mismatches: 13
 Query Match: 78.83% Indels: 1
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x PL0087 (1-120)

QY 1 CAGGTGAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCATC 60
 Db 1 GlnValGlnLeuLysArgSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGACTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCCGACGCT 120
 Db 21 ThrCysThrValSerGlyPheSerLeuThrSerSerGlyValHisTrpValArgGlnPro 40
 QY 121 CCAGAAAGGCTTCGAGTGGCTGGGAGTAATATGGACTGGTGGAGCAACAATATAAT 180
 Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAACAGCACTCCAGAGCCCAAGTTTCTTA 240
 Db 61 SerAlaLeuMetSerArgLeuThrIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAAATGAACAGTCTGCAGACTGAGCATCAGCAAAACAGCACTCCAGAGCCCAAGTTTCTTA 300
 Db 81 LysMetThrSerLeuGlnIleAspAspThrAlaMetTyrTyrCysAlaArgPhe 99
 QY 301 ACTATGATTAGGCTATGTATGAGTACTTGGGGCCAAAGGACCCAGGTCACCGTCTCC 360
 Db 100 HisCysGlyGlnAlaTyrGlyMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119
 QY 361 TCA 363
 Db 120 Ser 120

RESULT 5

S55028
 Ig heavy chain V region - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
 C/Accession: S55028
 R/Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff, R.; Mol. Biol. 248, 344-360, 1995
 A/Title: Structure and specificity of the anti-digoxin antibody 40-50.
 A/Reference number: S55027; MUID:95257394; PMID:7739045
 A/Accession: S55028
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-140 <UEF>
 A/Cross-references: EMBL:L31403; NID:g476717; PIDN:AAA38191.1; PID:g476718
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/34-116/Domain: immunoglobulin homology <IMW>

Alignment Scores:
 Pred. No.: 2,27e-44 Length: 140
 Score: 529.00 Matches: 100
 Percent Similarity: 88.43% Conservative: 7
 Best Local Similarity: 82.64% Mismatches: 14
 Query Match: 78.60% Indels: 0
 DB: 2 Gaps: 0

US-10-049-868A-2 (1-363) x S55028 (1-140)

QY 1 CAGGTGAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCATC 60
 Db 20 GlnValHisLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39
 QY 61 ACTTGACTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCCGACGCT 120
 Db 40 ThrCysThrValSerGlyPheSerLeuThrThrTyrGlyValHisTrpPheArgGlnPro 59

QY 121 CCAGAAAGGCTCTGGAGTGGCTGGGAGTAATATGAGTCTGGTGGAGCAACAATATAAT 180
 Db 60 ProGlyLysGlyLeuGluTrpLeuGlyLeuIleTrpAlaGlyGlnThrAspTyrAsn 79
 QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAACAGCACTCCAGAGCCCAAGTTTCTTA 240
 Db 80 SerAlaLeuMetSerArgLeuSerIleAsnLysAspAsnSerLysSerGlnValPheLeu 99
 QY 241 AAAATGAACAGTCTGCAGACTGAGCATCAGCAAAACAGCACTTACTGTGCAGAGATCGATCT 300
 Db 100 LysMetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgPhe 119
 QY 301 ACTATGATTAGGCTATGTATGAGTACTTGGGGCCAAAGGACCCAGGTCACCGTCTCC 360
 Db 120 AlaSerTyrTyrAspTyrAlaValAspTyrTrpGlyGlnGlyThrSerValThrValSer 139
 QY 361 TCA 363
 Db 140 Ser 140

RESULT 6

S11101
 Ig heavy chain V region (clone NQ2-48.2.2) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
 C/Accession: S11101
 R/Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
 Nature 304, 320-324, 1983
 A/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazone
 A/Reference number: S07331; MUID:83271467; PMID:6877353
 A/Accession: S11101
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-113 <XAA>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-97/Domain: immunoglobulin homology <IMW>

Alignment Scores:

Pred. No.: 3,59e-44 Length: 113
 Score: 527.00 Matches: 102
 Percent Similarity: 85.95% Conservative: 2
 Best Local Similarity: 84.30% Mismatches: 9
 Query Match: 78.31% Indels: 8
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11101 (1-113)

QY 1 CAGGTGAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuVal***ProSerGlnSerLeuSerIle 20
 QY 61 ACTTGACTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCCGACGCT 120
 Db 21 ThrCysThrValSerGly***SerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
 QY 121 CCAGAAAGGCTCTGGAGTGGCTGGGAGTAATATGAGTCTGGTGGAGCAACAATATAAT 180
 Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAACAGCACTCCAGAGCCCAAGTTTCTTA 240
 Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer***ValPheLeu 80
 QY 241 AAAATGAACAGTCTGCAGACTGAGCATCAGCAAAACAGCACTTACTGTGCAGAGATCGATCT 300
 Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
 QY 301 ACTATGATTAGGCTATGTATGAGTACTTGGGGCCAAAGGACCCAGGTCACCGTCTCC 360
 Db 101 Val-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
 QY 361 TCA 363
 Db 140 Ser 140

Db 113 Ala 113

RESULT 7
S11102
Ig heavy chain V region (clone NQ5-96.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11106
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11106
A:Molecule type: mRNA
A:Residues: 1-114 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.59e-44 Length: 114
Score: 527.00 Matches: 102
Percent Similarity: 85.95% Conservative: 2
Best Local Similarity: 84.30% Mismatches: 9
Query Match: 78.31% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11106 (1-114)

QY 1 CAGGTGACGTGCAGGAGTCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGlu***GlyProGlyLeuVal***ProSerGlnSerLeuSerile 20
QY 61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGTTACACTGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGly***SerLeuThrSerTyrglyValHisTrpValArgGlnPro 40
QY 121 CCAGAAAGGCTCTGGAGTGGCTGGAGTAATATGGACTGTGGTGAAGCACAAATATTAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTrpAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTrpAsn 60
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGTGAAGCACAAATATTAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTrpAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTrpAsn 60
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGTGAAGCACAAATATTAAT 180
Db 99 -----GlyPheAlaTyrrpGlyGlnGlyThrSerValThrValSer 112
QY 361 TCA 363
Db 113 Ser 113

RESULT 8
S11102
Ig heavy chain V region (clone NQ5-4.3.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11102
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11102
A:Molecule type: mRNA
A:Residues: 1-116 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 6.33e-44 Length: 139
Score: 524.50 Matches: 102
Percent Similarity: 89.17% Conservative: 5
Best Local Similarity: 85.00% Mismatches: 12
Query Match: 77.93% Indels: 1
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x A32456 (1-139)

QY 4 GTGCAGCTGCAGGAGTCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCTGTCCATC 63
Db 21 ValHisLeuLysGluSerGlyProValLeuValAlaProSerGlnSerLeuSerileThr 40
QY 64 TGCACCTGCTCTGGGATTTCATTAAACAGATATGTTACACTGGTTCGCCAGCCTCCA 123

Pred. No.: 3.58e-44 Length: 116
Score: 527.00 Matches: 102
Percent Similarity: 85.95% Conservative: 2
Best Local Similarity: 84.30% Mismatches: 9
Query Match: 78.31% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11102 (1-116)

QY 1 CAGGTGACGTGCAGGAGTCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuVal***ProSerGlnSerLeuSerile 20
QY 61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGTTACACTGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGly***SerLeuThrSerTyrglyValHisTrpValArgGlnPro 40
QY 121 CCAGAAAGGCTCTGGAGTGGCTGGAGTAATATGGACTGTGGTGAAGCACAAATATTAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTrpAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSer***ValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTrpAsn 60
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGTGAAGCACAAATATTAAT 180
Db 101 *****TyrrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113

RESULT 9

A32456

Ig heavy chain precursor V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

C:Accession: A32456

R:Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Badzyk, W.D.; Voss Jr., E.W.

J. Biol. Chem. 264, 4513-4522, 1989

A:Title: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin

A:Reference number: A32456; MUID:89174706; PMID:2494173

A:Accession: A32456

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <DOM>

A:Cross-references: GB:J04609; NID:G556316; PIDN:AAA50298.1; PID:G556317

A:Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 6.33e-44 Length: 139

Score: 524.50 Matches: 102

Percent Similarity: 89.17% Conservative: 5

Best Local Similarity: 85.00% Mismatches: 12

Query Match: 77.93% Indels: 1

DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x A32456 (1-139)

QY 4 GTGCAGCTGCAGGAGTCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCTGTCCATC 63

Db 21 ValHisLeuLysGluSerGlyProValLeuValAlaProSerGlnSerLeuSerileThr 40

QY 64 TGCACCTGCTCTGGGATTTCATTAAACAGATATGTTACACTGGTTCGCCAGCCTCCA 123


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181 TCGGCTCTCATGTCACAGACTGCAGCATCAGCAACAACTCCAAGAGCCCAAGTTTCTTA 240
|||||
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer***ValPheLeu 80
|||||
Qy 241 ARAATGAACAGCTCTGCAGACTGATGCACAGCCATGCTACTACTGTGCCAGAGATCGATCT 300
|||||
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
|||||
Qy 301 ACTATGATTACGGCCTATGCTATGCACTACTGGGGGCCAAGGGACCAACGGTCAACCGTCTCC 360
|||||
Db 101 Ala-----TyrTrpGly***GlyThrLeuValThrValSer 112
|||||
Qy 361 TCA 363
Db 113 Ala 113

RESULT 12
S11099
IG heavy chain V region (clone N02-17.4.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11099
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11099
A:Molecule type: mRNA
A:Residues: 1-114 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 5,54e-43 Length: 114

```

Score:	515.00	Matches:	100
Percent Similarity:	84.30%	Conservative:	2
Best Local Similarity:	82.64%	Mismatches:	11
Query Match:	76.52%	Indels:	8
DB:	2	Gaps:	1

US-10-049-868A-2 (1-363) x S11099 (1-114)

QY 1 CAGGTGCAGCTGCGAGAGCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCCGACGCT 120
Db 21 ThrCysThrValSerGly***SerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGAAAGGGTCTGGAGTGGAGTAAATATGAGTGGTGGAGGACACAAATATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCAGCATCAAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer***ValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATCACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAsp***Gly 100
QY 301 ACTATGATTACGGCCTATGCTATGAGTACTGGGCCCAAGGACACACGGTCCCGTCTCC 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeu***Thr***Ser 112
QY 361 TCA 363
Db 113 Ala 113

RESULT 13

Ig heavy chain V region (4B1 VH) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001

C:Accession: S42484

R:Gilbert, D.; Brard, F.; Margaritte, C.; Delpech, A.; Tron, F.

submitted to the EMBL Data Library, March 1994

A:Description: An idiotype D23-bearing polyclonal, murine anti-DNA monoclonal antibody

A:Reference number: S42484

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-116 <GIL>

A:Cross-References: EMBL:Z30962; NID:G461325; PIDN:CAA83216.1; PID:G461326

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3,07e-42 Length: 116
Score: 507.50 Matches: 98
Percent Similarity: 85.25% Conservative: 6
Best Local Similarity: 80.33% Mismatches: 11
Query Match: 75.41% Indels: 7
DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x S42484 (1-116)

QY 1 CAGGTGCAGCTGCGAGAGCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCCGACGCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrAlaIleSerTrpValArgGlnPro 40
QY 121 CCAGAAAGGGTCTGGAGTGGGTAATATGAGTGGTGGAGGACACAAATATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpThrGlyGlyThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCAGCATCAAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240

Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnIlePheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATCACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspAlaArgTyrPheCysAlaArgAsp----- 98
QY 301 ACTATGATTACGGCCTATGCT---ATGGACTACTGGGCCCAAGGACACACGGTCCCGTCC 357
Db 99 -----GlyTyrSerPheAspTyrTrpGlyGlnGlyThrLeuThrVal 114
QY 358 TCCTCA 363
Db 115 SerSer 116

RESULT 14

A49049

Ig heavy chain V region (anti-idiotypic) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C:Accession: A49049

R:Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.

Eur. J. Immunol. 22, 2893-2899, 1992

A:Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen

A:Reference number: A49049; MUID:93049629; PMID:1425914

A:Accession: A49049

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-122 <ARM>

A:Experimental source: BALB/c

A>Note: sequence extracted from NCBI backbone (NCBI:118295, NCBI:118296)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.51e-41 Length: 122
Score: 500.50 Matches: 99
Percent Similarity: 86.78% Conservative: 6
Best Local Similarity: 81.82% Mismatches: 13
Query Match: 74.37% Indels: 3
DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x A49049 (1-122)

QY 1 CAGGTGCAGCTGCGAGAGCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCCGACGCT 120
Db 21 ThrCysThrValSerGlyPheSerIleThrAspTyrValValSerTrpIleArgGlnPro 40
QY 121 CCAGAAAGGGTCTGGAGTGGGTAATATGAGTGGTGGAGGACACAAATATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyGlyGlyAsnThrTyrTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCAGCATCAAGCAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATCACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaLysHisAspGlu 100
QY 301 ACTATGATTACGGCCTATGCTATGAGTACTGGGCCCAAGGACACACGGTCCCGTCTCC 360
Db 101 -----IleThrThrTyr---PheAspTyrTrpGlyGlnGlyThrLeuThrValSer 117
QY 361 TCA 363
Db 118 Ser 118

RESULT 15

S26322
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C/Accession: S26322
R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26322
A:Molecule type: mRNA
A:Residues: 1-106 <STA>
A:Cross-references: EMBL:X59182
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F/9-91/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.7e-41 Length: 106
Score: 500.00 Matches: 97
Percent Similarity: 86.84% Conservative: 2
Best Local Similarity: 85.09% Mismatches: 7
Query Match: 74.29% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S26322 (1-106)

QY	19	TCTGGAGCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATCACTTGCACGTCTCTGGG	78
Db	1	SerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThrValSerGly	20
QY	79	ATTTCAITAAACAGATATGGTGTAACACTGGGTTCCGAGCCTCCAGGAAAGGGTCTGGAG	138
Db	21	PheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLysGlyLeuGlu	40
QY	139	TGGCTGGGAGTAATATGGAGCTGGTGGAGCACAAATTATATTCGGCTCTCATGTCCAGA	198
Db	41	TrpLeuGlyValIleTyrAlaGlyGlySerThrAsnTyrAsnSerAlaLeuMetSerArg	60
QY	199	CTGAGCATCAGCAAGAGCACTCCAGAGCCAGTTTCTTAAAAATGAACAGTCTGCAG	258
Db	61	LeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLysMetAsnSerLeuGln	80
QY	259	ACTGATCACACAGCCATGTACTACTGTGCCAGAGATCGATCTACTATGATTACGGCCCTAT	318
Db	81	ThrAspAspThrAlaMetTyrTyrCysAlaArgGlu-----	92
QY	319	GCTATGGAGTACTGGGGCCAGGAGGACCGGTACCGTCTCC	360
Db	93	AlaLeuArgLeuTrpGlyGlnGlyThrLeuValThrValSer	106

Search completed: October 13, 2004, 13:29:39
Job time : 23.6191 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_nzp model

Run on: October 13, 2004, 13:01:14 ; Search time 104.325 Seconds
(without alignments)
4004.053 Million cell updates/sec

Title: US-10-049-868A-2

Perfect score: 673

Sequence: 1 caggtgcagctcaggagtc.....ccaggtcaccgtctctccta 363

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+npz.model -DEV=xlp
-Q=/cgn2/1/USPTO.spool_P/US10049868/runat_13102004_132817_24791/app_query.fasta_1.1038
-DB=Uniprot_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 @CGN_1_1_305 @runat_13102004_132817_24791 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506.5	75.3	482	2 Q91X92	Q91X92 mus musculus
2	490.5	72.9	121	2 Q99NG4	Q99NG4 mus musculus
3	487	72.4	144	1 HV43 MOUSE	P01819 mus musculus
4	442	65.7	115	1 HV44 MOUSE	P01820 mus musculus
5	436	64.8	116	1 HV45 MOUSE	P01821 mus musculus
6	401.5	59.7	135	1 HV02 XENLA	P20957 xenopus lae
7	389.5	57.9	465	2 Q6GMX6	Q6GMX6 homo sapien
8	382	56.8	129	2 BAD00255	Bad00255 camelus d
9	376	55.9	119	2 Q9UL73	Q9UL73 homo sapien
10	373	55.4	121	1 HV3J HUMAN	P01771 homo sapien
11	371.5	55.2	620	2 Q96Y0	Q96Y0 homo sapien
12	366	54.4	476	2 Q6GMX1	Q6GMX1 homo sapien
13	364.5	54.2	477	2 Q6GMX7	Q6GMX7 homo sapien
14	364.5	54.2	576	2 Q6P418	Q6P418 homo sapien
15	364.5	54.2	576	2 AAH63384	AAH63384 homo sapi
16	364	54.1	137	1 HV46_MOUSE	P01822 mus musculus

17	361.5	53.7	124	2 BAD00233	Bad00233 camelus d
18	358.5	53.3	478	2 Q7Z379	Q7Z379 homo sapien
19	356.5	53.0	573	2 Q8WJ38	Q8WJ38 homo sapien
20	355	52.7	483	2 BAC85202	BAC85202 homo sapi
21	354	52.6	595	2 Q8WJX4	Q8WJX4 homo sapien
22	354	52.6	597	2 Q6GMX5	Q6GMX5 homo sapien
23	354	52.6	597	2 Q9BU10	Q9BU10 homo sapien
24	354	52.6	625	2 Q96AA6	Q96AA6 homo sapien
25	353.5	52.5	112	2 Q9HCC1	Q9HCC1 homo sapien
26	353	52.5	499	2 Q8NSK4	Q8NSK4 homo sapien
27	352	52.3	472	2 Q6N089	Q6N089 homo sapien
28	352	52.3	472	2 CAE45781	CAE45781 homo sapi
29	352	52.3	501	2 BAC85359	BAC85359 homo sapi
30	351	52.2	136	1 HV01 XENLA	P20956 xenopus lae
31	350	52.0	120	2 BAD00465	Bad00465 camelus d
32	350	52.0	128	2 BAD00406	Bad00406 camelus d
33	348.5	51.8	122	1 HV3G HUMAN	P01768 homo sapien
34	348	51.7	597	2 Q9BQB8	Q9BQB8 homo sapien
35	347	51.6	479	2 BAC85434	BAC85434 homo sapi
36	346	51.4	470	2 BAC85387	BAC85387 homo sapi
37	345.5	51.3	118	2 Q811U5	Q811U5 mus musculu
38	344.5	51.2	613	2 Q8WUK1	Q8WUK1 homo sapien
39	343	51.0	139	2 Q86SX2	Q86SX2 homo sapien
40	342.5	50.9	120	2 AAL35864	AAL35864 lama glam
41	341.5	50.7	136	2 Q6LBQ5	Q6LBQ5 mus musculu
42	341.5	50.7	136	2 CA34714	CA34714 mus muscu
43	341	50.7	472	2 BAC85393	BAC85393 homo sapi
44	340	50.5	254	2 BAC86524	BAC86524 homo sapi
45	339.5	50.4	494	2 BAC85198	BAC85198 homo sapi

ALIGNMENTS

RESULT 1

Q91X92	Q91X92	PRELIMINARY;	PRT;	482 AA.
ID	Q91X92			
AC	Q91X92;			
DT	01-DEC-2001 (T-EMBLrel. 19, Created)			
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)			
DE	Igh-VJ558 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RC	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McWayne P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RA	Strausberg R.;			

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC011181; AAH11181.1; --
 DR PIR; F33932; F33932.
 DR HSSP; P01820; IATN.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; CI-set; 2.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 482 AA; 51864 MW; 31ZE01F9C1BC7F3C CRC64;

Alignment Scores:
 Pred. No.: 4,366-48 Length: 482
 Score: 506.50 Matches: 100
 Percent Similarity: 86.18% Conservative: 6
 Best Local Similarity: 81.30% Mismatches: 10
 Query Match: 75.26% Indels: 7
 DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x Q91X92 (1-482)

QY 1 CAGGTGACGTGACGAGCTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
 Db 20 GlnValGlnLeuLysGluSerGlyProAspLeuValAlaProSerGlnSerLeuSerile 39
 QY 61 ACTTGCACTGCTCTCGGATTTCATTAAACAGATATGGTGACACTGGGTTGCCAGCCT 120
 Db 40 ThrCysThrValSerGlyPheAlaLeuThrSerTyrAlaIleSerTrpValArgGlnPro 59
 QY 121 CCAGGAAGGCTCTGGAGTGGCTGGAGTAATATGGAGTGGTGGNAGGACAAATATAAT 180
 Db 60 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpThrGlyValThrAsnTyrAsn 79
 QY 181 TCGGCTCTCATGTCAGACTGACATCAGCAAGCAACTCCAGAGGCCAAGTTTCTTA 240
 Db 80 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 99
 QY 241 AAATGAAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
 Db 100 LysMetAsnSerLeuGlnThrAsnAspThrAlaArgTyrTyrCysAlaArgSerAsn 119
 QY 301 ACTATGATTACGGCTAT-----GCTATGCACTCTGGGCGCCAGGACACCGTCAAC 354
 Db 120 -----TyrGluGlyAlaMetAspTyrTrpGlyGlnGlyThrSerValThr 134
 QY 355 GTCTCTCTCA 363
 Db 135 ValSerSer 137

RESULT 2

Q91X92 PRELIMINARY; PRT; 121 AA.
 AC Q91X92;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Single chain Fv (Fragment).
 OS Mus musculus (Mouse).
 OG Plasmid pHENi.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=98169018; PubMed=95101199;
 RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
 RA Bausch W., Kola A., Klos A., Koehl J.;
 RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";

J. Immunol. 160:2947-2958(1998).
 DR EMBL; AJ222590; CAA10890.1; --
 DR PIR; F33932; F33932.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Plasmid.
 FT NON_TER 1 121
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13255 MW; D293E4EB8C59D5B CRC64;

Alignment Scores:

Pred. No.: 2,32e-46 Length: 121
 Score: 490.50 Matches: 96
 Percent Similarity: 85.95% Conservative: 8
 Best Local Similarity: 79.34% Mismatches: 16
 Query Match: 72.88% Indels: 1
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x Q99NG4 (1-121)

QY 1 CAGGTGACGTGACGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
 QY 61 ACTTGCACTGCTCTCGGATTTCATTAAACAGATATGGTGACACTGGGTTGCCAGCCT 120
 Db 21 ThrCysThrValSerGlyPheProLeuThrSerHisGlyValSerTrpValArgGlnPro 40
 QY 121 CCAGGAAGGCTCTGGAGTGGCTGGAGTAATATGGAGTGGTGGNAGGACAAATATAAT 180
 Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlyAsnThrLysTyrHis 60
 QY 181 TCGGCTCTCATGTCAGACTGACATCAGCAAGCAACTCCAGAGGCCAAGTTTCTTA 240
 Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAATGAAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
 Db 81 LysLeuAsnSerLeuGlnThrGluAspThrAlaThrTyrTyrCysAlaArg---HisTyr 99
 QY 301 ACTATGATTACGGCTATGTCTATGCACTCTGGGCGCCAGGACACCGTCAACGCTCC 360
 Db 100 TyrLysTyrAlaAsnTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119
 QY 361 TCA 363
 Db 120 Ser 120

RESULT 3

HV43_MOUSE STANDARD; PRT; 144 AA.
 ID HV43_MOUSE
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Ig heavy chain V region MOPC 141 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes.";
 RL Nature 286:676-683(1980).
 CC -!- MISCELLANEOUS: The sequence shown is translated from a
 CC differentiated gene isolated from a myeloma that secretes IgG2b.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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 CC -----

EMBL; J00491; AAA38121.1; -;
 DR PIR; A02094; G2MS14.
 DR HSSP; P01820; IG7J.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144 Ig heavy chain V region MOPC 141.
 FT DOMAIN 20 130 Ig-like.
 FT NON_TER 144
 SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Alignment Scores:
 Pred. No.: 5, 92e-46 Length: 144
 Score: 487.00 Matches: 97
 Percent Similarity: 81.25% Conservative: 7
 Best Local Similarity: 75.78% Mismatches: 14
 Query Match: 72.36% Indels: 10
 DB: 1 Gaps: 2

US-10-049-868A-2 (1-363) x HV43_MOUSE (1-144)

QY 1 CAGTGCAGCTGCAGGAGCTGCAGCTGGCTGGTGGCGCCCTCACAGACCTGTCCATC 60
 Db 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39
 QY 61 ACTTGCACTCTCTGGATTTCATTAACAGATATGCTACATGGTTCGCCAGCCT 120
 Db 40 ThrCysThrValSerGlyPheSerLeuThrGlyValAsnTrpValArgGlnPro 59
 QY 121 CCAGGAAGGCTCGGAGTGGCTGGGAGTAAATGGACTGGTGAAGCACAAATTATAAT 180
 Db 60 ProGlyLysGlyLeuGluTrpLeuGlyThrIleTrpGlyAsnGlySerThrAspTyrAsn 79
 QY 181 TCGGCTCTCATGTCCAGACTGACATCAGCAACAGCAACTCCAGAGCCCAAGTTTCTTA 240
 Db 80 SerThrLeuLysSerArgLeuThrIleThrLysAspAsnSerLysSerGlnValPheLeu 99
 QY 241 ABAATGACAGCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
 Db 100 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAla-----Ser 116
 QY 301 ACTATGATTACGGCCAT-----GCTATGGACTACTGGGGCAA 339
 Db 117 ValSerIleTyrTyrTyrGlyArgSerAspLysTyrPheThrLeuAspTyrTrpGlyGln 136
 QY 340 GGGACACAGGTACCGTCTCTCTCA 363

Db 137 GlyThrSerValThrValSerSer 144

RESULT 4

HV44_MOUSE
 ID HV44_MOUSE STANDARD; PRT; 115 AA.
 AC P01820;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig heavy chain V region P14 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 RL of complete immunoglobulin heavy-chain genes.";
 Nature 286:676-683(1980).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----

EMBL; V00767; CAA24148.1; -;
 DR PIR; A02095; HVMS14.
 DR PDB; 1A7N; X-ray; H=20-115.
 DR PDB; 1A7O; X-ray; H=20-115.
 DR PDB; 1A7P; X-ray; H=20-115.
 DR PDB; 1A7R; X-ray; H=20-115.
 DR PDB; 1G7H; X-ray; B=20-115.
 DR PDB; 1G7I; X-ray; B=20-115.
 DR PDB; 1G7J; X-ray; B=20-115.
 DR PDB; 1G7N; X-ray; B=20-115.
 DR PDB; 43C9; X-ray; B/D/F/H=19-115.
 DR PDB; 43CA; X-ray; B/D/F/H=20-115.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW 3D-structure; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 115 Ig heavy chain V region P14.
 FT DOMAIN 20 >115 Ig-like.
 FT STRAND 22 26
 FT STRAND 30 30
 FT STRAND 37 44
 FT TURN 48 49
 FT STRAND 52 58
 FT TURN 60 61
 FT STRAND 65 70
 FT TURN 72 73
 FT STRAND 76 78
 FT TURN 80 82
 FT STRAND 83 85
 FT STRAND 86 91
 FT HELIX 92 94
 FT TURN 95 95
 FT STRAND 96 101
 FT HELIX 106 108
 FT STRAND 110 115
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Alignment Scores:
 Pred. No.: 7, 13e-41 Length: 115
 Score: 442.00 Matches: 85
 Percent Similarity: 92.71% Conservative: 4
 Best Local Similarity: 88.54% Mismatches: 7
 Query Match: 65.68% Indels: 0
 DB: 1 Gaps: 0

US-10-049-868A-2 (1-363) x HV44_MOUSE (1-115)

QY 1 CAGTGCAGCTGCAGGAGCTGCAGCTGGCTGGTGGCGCCCTCACAGACCTGTCCATC 60
 Db 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39

QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGTTACACTGGGTTTCGCCAGCCT 120
 |||||
 Db 40 ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAlaSerTrpValArgGlnPro 59
 |||||
 QY 121 CCAGGAAGGCTCTGGAGTGGCTGGAGTAAATATGAGTGGTGGAGCACAATATATAAT 180
 |||||
 Db 60 ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlySerThrAspTyrAsn 79
 |||||
 QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCCAGAGCCAGAGTTTCTTA 240
 |||||
 Db 80 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 99
 |||||
 QY 241 AAAATGAACAGCTCTGCAGACTGATGACACAGCCATGTACTACTGTGCC 288
 |||||
 Db 100 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAla 115
 |||||

RESULT 5

HV45_MOUSE
 ID HV45_MOUSE STANDARD; PRT; 116 AA.
 AC P01821;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MC101 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82075900; PubMed=6273429;
 RA Kataoka T., Nikaido T., Miyata T., Moriaki K., Honjo T.;
 RT "The nucleotide sequences of rearranged and germ-line immunoglobulin VH
 RT genes of a mouse myeloma MC101 and evolution of VH genes in mouse."
 RL J. Biol. Chem. 257:277-285 (1982).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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 CC EMBL; J00502; AAA38515.1; -;
 DR PIR; A02096; GIMS10.
 DR HSSP; P01820; IG7J.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT CHAIN 20 116 Ig heavy chain V region MC101.
 FT DOMAIN 20 >116 Ig-like.
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;

Alignment Scores:

Pred. No.: 3,41e-40 Length: 116
 Score: 436.00 Matches: 81
 Percent Similarity: 92.78% Conservative: 9
 Best Local Similarity: 83.51% Mismatches: 7
 Query Match: 64.78% Indels: 0
 DB: 1 Gaps: 0

US-10-049-868A-2 (1-363) x HV45_MOUSE (1-116)

QY 1 CAGGTGACAGTCGAGGACTGGACCTGGCTGGTGGCGCCCTCAGACAGCCTGTCCATC 60
 |||||
 Db 20 GlnValGlnLeuLysGlnSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIle 39
 |||||

QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGTTACACTGGGTTTCGCCAGCCT 120
 |||||
 Db 40 ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAlaSerTrpValArgGlnSer 59
 |||||
 QY 121 CCAGGAAGGCTCTGGAGTGGCTGGAGTAAATATGAGTGGTGGAGCACAATATATAAT 180
 |||||
 Db 60 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyGlySerThrAspTyrAsn 79
 |||||
 QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCCAGAGCCAGAGTTTCTTA 240
 |||||
 Db 80 AlaAlaPheIleSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhePhe 99
 |||||
 QY 241 AAAATGAACAGCTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGA 291
 |||||
 Db 100 LysMetAsnSerLeuGlnSerAsnAspThrAlaIleTyrTyrCysAlaArg 116
 |||||

RESULT 6

HV02_XENLA
 ID HV02_XENLA STANDARD; PRT; 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88176921; PubMed=2451244;
 RA Schwager J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
 RT from cDNA sequence: implications for evolution of immunoglobulin
 RT domains."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249 (1988).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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 CC EMBL; J03632; AAA49791.1; -;
 DR PIR; B31933; B31933.
 DR HSSP; P01820; 1A7N.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1
 FT NON TER 1 1
 FT CHAIN 19 135 Ig heavy chain V region XIG14.
 FT DOMAIN 20 128 Ig-like.
 FT NON TER 135 135
 SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Alignment Scores:

Pred. No.: 2,8e-36 Length: 135
 Score: 401.50 Matches: 73
 Percent Similarity: 77.97% Conservative: 19
 Best Local Similarity: 61.86% Mismatches: 23
 Query Match: 59.66% Indels: 3
 DB: 1 Gaps: 1

US-10-049-868A-2 (1-363) x HV02_XENLA (1-135)


```

QY 10 CTGCAGGAGTCTGACCTGGCTGGTGGCGCCCTCAGAGCCCTGTCATCCTGCACT 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 LeuGlnGluSerGlyProGlyThrValLysProSerGluSerLeuArgLeuThrCysThr 40
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 GTCTCTGGATTTCATTAACAGATATGTTACATCGGTTCGCCAGCTCCAGGAAAG 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 ValSerGlyPheGluLeuSerSerTyHisMetHisTrpIleArgGlnProProGlyLys 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 130 GGTCTGAGTGGCTGGAGTAATATGACTGGTGGAGCAGCAAAATTATATTCGGTCTC 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GlyLeuGluTrpIleGlyValIleAlaThrGlyGlySerThrAlaIleAlaAspSerLeu 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 ATGTCCAGACATGACATCAGCAAAAGACATCCCAAGAGCCCAAGTTTCTTAARATGAAC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 LysAsnArgValThrIleThrLysAspAsnGlyLysGlnValTyLeuGlnMetCasn 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 250 AGTCTGAGACTGATGACAGACCATGATCTACTGTCGCCAGAGATCGATCTATGATT 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 GlyMetGluValLysAspThrAlaMetTyTrpCysAlaArgGluTyAla----- 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 310 ACGGCTATGCTATGGACTACTGGGCGCAAGGACACCGTCACCGTCTCTCTCA 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 SerGlyTyraAsnPheAspTyTrpGlyGlnGlyThrMetValThrValThrSer 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalley D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
PFam; PF07654; C1-set; 3.

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DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein_
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Alignment Scores:
Pred. No.: 7,63e-35 Length: 465
Score: 389.50 Matches: 76
Percent Similarity: 76.86% Conservative: 17
Best Local Similarity: 62.81% Mismatches: 23
Query Match: 57.88% Indels: 5
DB: Gaps: 1

US-10-049-868A-2 (1-363) x Q6GMX6 (1-465)
QY 1 CAGTGCAGCTGCGAGGAGTCTGGACCTGGCTGGCGCCCTCAGAGCCCTGTCATC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 39
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 ACTTGCACCTCTCTGGGATTTCATTAACAGATATGCTACACTGGTTCGCCAGCCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 ThrCysThrValSerGlyGlySerIleSerGlyTyTrpSerTrpIleArgGlnPro 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CCAGAAAGGCTCTGGAGTGGCTGGGAGTAATATGCACTGGTGGAGCAGCAAAATTATAAT 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 AlaGlyLysGlyLeuGluTrpIleGlyArgIleTyThrSerGlySerThrAsnTyra 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TCGGCTCTCATGTCAGACTGACATCAGCAAAAGACAACTCCAGAGCCCAAGTTTCTTA 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 ProSerLeuLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeu 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AAAATGAACAGTCTGCAGACTGATGATGACAGCCATGCTACTGCTGGCAGAGATCGATCT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 100 LysLeuSerSerValThrAlaAlaAspThrAlaValTyTrpCysAlaArgGlyArgPhe 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 ACTATGATTACGGCTATGCTATGGAATCTGCTGGGCGCAAGGACCGGTCACCGTCTCC 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 ThrTyrr-----PheAspTyTrpGlyGlnGlyThrLeuValThrValSer 134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 TCA 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 Ser 135

RESULT 8
BAD00255 PRELIMINARY; PRT; 129 AA.
AC BAD00255
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091893; BAD00255.1; -.
FT NON_TER 1
FT NON_TER 129
SQ SEQUENCE 129 AA; 14117 MW; D9642F5A5BE3BEE CRC64;

Alignment Scores:

```

Pred. No.: 4.49e-34 Length: 129
 Score: 382.00 Matches: 75
 Percent Similarity: 73.64% Conservative: 20
 Best Local Similarity: 58.14% Mismatches: 26
 Query Match: 56.76% Indels: 8
 DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x BAD00255 (1-129)

QY 1 CAGGTGAGCTGCAGGAGCTGGAGCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
 |||||
 Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnThrLeuThrLeu 20
 |||||
 QY 61 ACTTGCACCTGCTCTGGG-----ATTTCATTAAACAGATATGGTGACACTGGGTTCCG 114
 |||||
 Db 21 ThrCysThrValSerGlySerIleThrThrSerTyrTyrGlyTyrPheSerTrpIleArg 40
 |||||
 QY 115 CAGCTCCAGGAAGGGTCTGGAGTGGCTGGGAGTAATATGAGCTGGTGGAGACACAAT 174
 |||||
 Db 41 GlnProProGlyLysGlyLeuGluTrpMetGlyAlaIleAlaTyrSerGlySerThrTyr 60
 |||||
 QY 175 TATATTCGGCTTCATCTCAGACTGAGCATCAGCAAGACAACTCCAGAGCCCAAGTT 234
 |||||
 Db 61 TyrSerProSerLeuLysSerArgThrSerPheSerArgAspThrSerLysAsnGlnPhe 80
 |||||
 QY 235 TTCTTAAAAATGAACAGTCTCAGACTGATGACAGCCATGCTACTGTCGCCAGAGAT 294
 |||||
 Db 81 SerLeuGlnLeuSerSerValThrProGluAspThrAlaValTyrCysAlaArgAsp 100
 |||||
 QY 295 CGA-----TCTACTATGATTACGGCTATGCTATGCTATGCTATGCTATGCTATGCT 336
 |||||
 Db 101 SerProArgLeuArgValGlySerGluSerArgGlyValTyrSerMetAspTyrTrpGly 120
 |||||
 QY 337 CAAGGACCACGGTCACCGTCTCCTCA 363
 |||||
 Db 121 LysGlyThrLeuValThrIleSerSer 129

RESULT 9

QYUL73 PRELIMINARY; PRT; 119 AA.
 AC QYUL73;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035041; AAD56277.1; -.
 DR PIR; PH0876; PH0876.
 DR PIR; S12416; S12416.
 DR HSSP; P01820; 1G7J.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON TER 119
 FT NON TER 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EACBE CRC64;

Alignment Scores:
 Pred. No.: 2.12e-33 Length: 119
 Score: 376.00 Matches: 75

Percent Similarity: 74.38% Conservative: 15
 Best Local Similarity: 61.98% Mismatches: 29
 Query Match: 55.87% Indels: 2
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x Q9UL73 (1-119)

QY 1 CAGGTGAGCTGCAGGAGCTGGAGCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
 |||||
 Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeu 20
 |||||
 QY 61 ACTTGCACCTGCTCTGGGATTTCATTAAACAGATATGGTGACACTGGGTTCCGAGCCT 120
 |||||
 Db 21 ThrCysThrValSerGlyGlySerIleCysSerTyrTyrTrpSerTrpIleArgGlnPro 40
 |||||
 QY 121 CCAGGAAGGGTCTGGAGTGGCTGGGAGTAATATGAGCTGGTGGAGACACAATATAAT 180
 |||||
 Db 41 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrThr 60
 |||||
 QY 181 TCGGCTCTCATGCTCAGACTGAGCATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTA 240
 |||||
 Db 61 ProSerLeuLysSerArgValThrIleSerValAspArgSerLysAsnGlnPheSerLeu 80
 |||||
 QY 241 AAAATGAACAGTCTGCAGACTGATGACAGCCATGCTACTGTCGCCAGAGATCGATCT 300
 |||||
 Db 81 LysLeuThrSerLeuThrAlaAlaAspThrAlaValTyrPheCysAla-----ArgLeu 98
 |||||
 QY 301 ACTATGATTACGGCTATGCTATGAGCTACCTGGGCGCCAGGACACCGTCCACGCTCTCC 360
 |||||
 Db 99 SerAsnTrpGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 118
 |||||
 QY 361 TCA 363
 |||||
 Db 119 Ser 119

RESULT 10

HV3J HUMAN
 ID HV3J HUMAN STANDARD; PRT; 121 AA.
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region HIL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RA "Amino acid sequence of the VH region of human myeloma
 RT cryoimmunoglobulin IgG Hil.";
 RL Biochemistry 18:553-560 (1979).
 CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
 CC protein.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02054; G1HUHL.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KW Pyrolydione carboxylic acid.
 FT DOMAIN 1 112 IG-like.
 FT MOD_RES 1 1 Pyrolydione carboxylic acid.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;


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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Alignment Scores:
Pred. No.: 3.5e-32 Length: 476
Score: 366.00 Matches: 78
Percent Similarity: 71.32% Conservative: 14
Best Local Similarity: 60.47% Mismatches: 27
Query Match: 54.38% Indels: 10
DB: 2 Gaps: 3

US-10-049-868a-2 (1-363) x QCGMX1 (1-476)
QY 1 CAGGTGACGTGACGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 20 GlnValGlnLeuGlnGlnSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeu 39
QY 61 ACTTGCACTGTCTCTGGG-----ATTTCATTAACACAGATATGGGTACACTGGGTCGC 114
Db 40 ThrCysThrValSerGlyGlySerGlySerGlyAspTyrTyrTrpSerTrpIleArg 59
QY 115 CAGCTTCAGGAAGGCTCTGGAGTGGCTGGGAGTAATATGACTGGTGGAGACCAAT 174
Db 60 GlnProProGlyGlyGlyLeuGlnTrpIleGlyTyrIleTyrTyrSerGlySerThrTyr 79
QY 175 TATAATTCGGCTCTCATGTCCAGACTGACATCAGCAAGACAACTCCCAAGACCAAGTT 234
Db 80 TyrAsnProSerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnGlnPhe 99
QY 235 TTCTTAAANAATGAACAGTGTGCAGACTGATGATGACACAGCCATGCTACTGTGCCAGAGAT 294
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Db 100 SerLeuLysMetAsnSerValThrAlaAlaAspThrAlaValTyrPheCysAlaArgAla 119
QY 295 -----CGATCTACTATGATTACGGCTATGCTATGCTATGCTACTTGGGGC 336
Db 120 GlyValTrpGlySerPheArgSerTrpAlaIleAspGlyPhe-----AsileTrpGly 137
QY 337 CAAGGACCCAGCGTCACCGTCTCCTCA 363
Db 138 GlnGlyThrMetValThrValSerSer 146

RESULT 13
QCGMX7 PRELIMINARY; PRT; 477 AA.
ID Q6GMX7
AC Q6GMX7;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Alignment Scores:
Pred. No.: 5.18e-32 Length: 477
Score: 364.50 Matches: 72
Percent Similarity: 73.55% Conservative: 17
Best Local Similarity: 59.50% Mismatches: 29
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Query Match: 54.16% Indels: 3
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x Q6GMX7 (1-477)

QY 1 CAGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCTGGCCCTCACAGAGCCTGTCATC 60
   |||||
Db 20 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 39
   |||||

QY 61 ACTTGCACTGCTCTGGATTTCATTAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
   |||||
Db 40 ThrCysThrValSerGlyGlySerIleSerSerYrYrTrpSerTrpIleArgGlnThr 59
   |||||

QY 121 CCAGGAAGGCTCGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCAACAAATTAAT 180
   |||||
Db 60 AlaGlyLysGlyLeuGluThrIleGlyYrYrIleSerHisSerGlySerThrThrYrAsn 79
   |||||

QY 181 TCGCTCTCATGTCAGACATGAGCATCAGCAAGCAACATCCAGAGCCCAAGTTTCTTA 240
   |||||
Db 80 ProSerLeuLysSerArgValThrLeuSerLeuAspThrSerLysAsnGlnPheSerLeu 99
   |||||

QY 241 AAAATGACAGCTGCAGAGCTGATGACACAGCCATGACTACTGTGCCAGAGATCGATCT 300
   |||||
Db 100 ArgLeuAsnSerValThrAlaAlaAspThrAlaValTyrCysAlaHisGlySerSer 119
   |||||

QY 301 ACTATGATTACGGCCTATGCTATGCACTACTGGGGCCAGGACACCGGTCCCGTCTCC 360
   |||||
Db 120 -----TrpAspPheAlaPheAspYrTrpGlyGlnGlyThrLeuValThrValSer 136
   |||||

QY 361 TCA 363
   |||||
Db 137 Ser 137

RESULT 14
Q6P418
ID Q6P418 PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettum A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gramwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnertch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;

```

```

RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_NHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_NHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.: 5,32e-32 Length: 576
Score: 364.50 Matches: 76
Percent Similarity: 73.77% Conservative: 14
Best Local Similarity: 62.30% Mismatches: 29
Query Match: 54.16% Indels: 3
DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x Q6P418 (1-576)
QY 1 CAGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCTGGCCCTCACAGAGCCTGTCATC 60
   |||||
Db 27 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlyThrLeuSerLeu 46
   |||||

QY 61 ACTTGCACTGCTCTGGATTTCATTAACAGATATGGT---GTACACTGGGTTCGCCAG 117
   |||||
Db 47 ThrCysAlaValSerGlyGlySerIleSerSerAsnTrpTrpSerTrpValArgGln 66
   |||||

QY 118 CTCTCCAGAAAGGCTGGAGTGGCTGGAGTAGTAATATGGACTGGTGGAGCAACAAATTA 177
   |||||
Db 67 ProProGlyLysGlyLeuGluThrIleGlyGluIleYrHisSerGlySerThrAsnYr 86
   |||||

QY 178 AATTCCGCTCTCATGTCCAGACTGAGCATCAGCAAGCAACATCCAGAGCCCAAGTTTTC 237
   |||||
Db 87 AsnProSerLeuLysSerArgValThrIleSerValAspLysSerLysAsnGlnPheSer 106
   |||||

QY 238 TTAATAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCGCAGAGATCGA 297
   |||||
Db 107 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAlaSerLeuGly 126
   |||||

QY 298 TCTACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAGGACCCAGGTCCCGTC 357
   |||||
Db 127 Asp-----IleYrYrYrGlyMetAspValTrpGlyGlnGlyThrThrValThrVal 144
   |||||

QY 358 TCCTCA 363
   |||||
Db 145 SerSer 146

RESULT 15
AAH63384
ID AAH63384 PRELIMINARY; PRT; 576 AA.
AC AAH63384;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettum A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gramwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnertch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;

```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:

Pred. No.:	5.32e-32	Length:	576
Score:	364.50	Matches:	76
Percent Similarity:	73.77%	Conservative:	14
Best Local Similarity:	62.10%	Mismatches:	29
Query Match:	54.16%	Indels:	3
DB:	2	Gaps:	2

US-10-049-868A-2 (1-363) x AAH63384 (1-576)

QY	1	CAGGTGACGTGACGAGTCTGGACCTGGCTGGCGCCTCACAGAGCTGTCCATC	60
Db	27	GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlyThrLeuSerLeu	46
QY	61	ACTTGCACTGTCTCTGGGATTCTAATAACAGATATGGT--GTACACTGGGTTCCGCG	117
Db	47	ThrCysAlaValSerGlyGlySerIleSerSerSerAsnTrpTrpSerTipValArgGln	66
QY	118	CCTCCAGGAAGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGCACAAATTAT	177
Db	67	ProProGlyLysGlyLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyr	86
QY	178	AATTCGGCTCTCATCTCCAGACTGAGCATCAAGAAAGCAACTCCAGAGCCCAAGTTTC	237
Db	87	AsnProSerLeuLysSerArgValThrIleSerValAspLysSerLysAsnGlnPheSer	106
QY	238	TTAAAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGATCGA	297
Db	107	LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerLeuGly	126
QY	298	TCTACTATGATTACGGCTATGCTATGACTACTGGGCGCCAGGACCGTCCACCGTC	357
Db	127	Asp-----IleTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThrValThrVal	144
QY	358	TCCTCA 363	
Db	145	SerSer 146	

Search completed: October 13, 2004, 13:28:08
Job time : 107.325 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:00:14 ; Search time 82.9571 Seconds

(without alignments)
3139.425 Million cell updates/sec

Title: US-10-049-868A-2

Perfect score: 673

Sequence: 1 caggtcagctgcagagtc.....ccacgtccagctctctca 363

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool_p/US10049868/runat_13102004_132816_24785/app_query.fasta_1.1038
-DB=A_Geneseq_23Sep04 -QFMT=fastan -SUFFIX=tag -MINMATCH=0.1 -LOOPCf=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868@cgn_1_1_308@runat_13102004_132816_24785 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	82.8	113	2	AAR21268 Murine VH
2	555	82.5	115	8	ADF77174 Anti-VAP-
3	553	82.2	125	6	ABR44627 Murine va
4	547	81.3	667	6	ABP97414 Anti-huma
5	546	81.1	253	5	Aau72867 P5-9 sing
6	541.5	80.5	120	4	AA663986 Amino aci
7	538	79.9	222	2	AA32843 VH NQ2/12
8	538	79.9	235	2	AA32840 VH NQ2/12
9	537	79.8	142	4	AA66520 Mouse ant
10	535	79.5	119	2	AA49218 Heavy cha

11	535	79.5	119	6	ADA14778	Adal4778 Peptide f
12	535	79.5	119	7	ADC35320	Adc35320 Anti-Idio
13	534	79.3	123	2	AAW07438	AAW07438 Anti-DNA
14	534	79.3	269	2	AAR32569	Aar32569 Fusion pr
15	532	79.0	476	4	AAAB49243	Aab49243 Chimeric
16	531.5	79.0	140	2	AAW22538	Aaw22538 Murine an
17	531.5	79.0	140	5	AAE20201	Aae20201 Murine 44
18	531.5	79.0	140	8	ADJ31875	Adj31875 Murine 44
19	526	78.2	119	5	AAU72838	Aau72838 Anti-NKG2
20	525.5	78.1	242	2	AAR06483	Aar06483 18-2-3-/T
21	525.5	78.1	242	2	AAAR43680	Aar43680 Single ch
22	525.5	78.1	242	2	AAR99650	Aar99650 Single ch
23	525.5	78.1	242	2	AAW02192	Aaw02192 18-2-3/TR
24	523	77.7	119	2	AAW42451	Aaw42451 Mouse ant
25	522.5	77.6	247	8	ADG28588	Adg28588 Paramyxov
26	522.5	77.6	287	6	ABR42057	Ab42057 Costimula
27	521.5	77.6	543	7	ADD12876	Add12876 CD28/mela
28	521.5	77.5	112	2	AAW31648	Aaw31648 Monoclonal
29	521.5	77.5	239	2	AAW02191	Aaw02191 18-2-3/TR
30	521.5	77.5	241	2	AAAR06482	Aar06482 18-2-3-/T
31	521	77.4	121	7	ADD25691	Add25691 Binding d
32	521	77.4	271	7	ADD25693	Add25693 Binding d
33	521	77.4	556	7	ADD25707	Add25707 Binding d
34	520.5	77.3	239	2	AAAR43679	Aar43679 Single ch
35	520.5	77.3	239	2	AAAR9649	Aar9649 Single ch
36	519	77.1	119	6	ABJ19263	Abj19263 Anti-huma
37	519	77.1	279	6	ABJ19275	Abj19275 Anti-huma
38	518.5	77.0	116	2	AAAR40951	Aar40951 Mouse ger
39	518	77.0	119	2	AAAR98478	Aar98478 MAB 2B6 h
40	517.5	76.9	116	4	AAU07513	Aau07513 Antibody
41	517.5	76.9	239	2	AAW09813	Aaw09813 Vllys-lin
42	517.5	76.9	239	2	AAW35561	Aaw35561 ECoR1-Hin
43	517.5	76.9	241	2	AAAR21261	Aar21261 VHD1.3-Hu
44	517.5	76.9	267	2	AAAR04841	Aar04841 Two linke
45	517.5	76.9	272	2	AAAR21260	Aar21260 ScFv sequ

ALIGNMENTS

RESULT 1

AAAR21268

ID AAR21268 standard; protein; 113 AA.

AC AAR21268;

DT 21-MAY-1992 (first entry)

DE Murine VH group 2 chain E specific for phOx.

FW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;

KK g3p; binding; adsorption; gene VIII; diverse repertoire;

KW specific binding pairs; replicable genetic display package.

OS Synthetic.

PH Key

FT Binding-site

FT Binding-site

FT Binding-site

FT Binding-site

FT Binding-site

FT Binding-site

FT /note= "D/N-X-G-X-X motif "

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990;

XX 10-JUL-1990;

XX 19-OCT-1990;

XX 12-NOV-1990;

XX 90GB-00024503.

PR 06-MAR-1991; 91GB-00004744.
 PR 15-MAY-1991; 91GB-00010549.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MED RES COUNCIL.
 XX
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD;
 XX
 DR WPI; 1992-056862/07.
 XX

PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic display
 PT package.
 XX

PS Example 21; Fig 24; 209pp; English.
 XX

CC The VH sequence is one of eight (AAR21264-71) found to be expressed from
 CC a single chain Fv library from an immunised mouse. The library produces a
 CC diverse repertoire of antibody fragments specific for 2-phenyl-5-
 CC oxazolone (phOx). It was prepd. using cDNA generated from mRNA from mice
 CC immunised with phOx coupled to chicked serum albumin. The VH and VL kappa
 CC sequences were separately amplified by PCR (see AAQ23474-84) and ligated
 CC into fCART2 (see AAQ23463) for expression on the phage surface as fusions
 CC with gene III. The resulting library of clones was diverse. Twenty three
 CC hapten binding clones were sequenced revealing the eight different VH
 CC genes (A-H) in a variety of pairings with seven different Vk genes (a-g)
 CC (see AAR21264-92). Nearly all the VH genes belonged to gp 1, with only
 CC one, "E", being of gp 2 (VHox1). Of the twenty three clones sequenced,
 CC only one was of type "E". Most of the clones were Vk-d combinations. The
 CC Kd of VH-B/Vk-d for phOx-GABA was 10 nM. Only two other combinations (of
 CC eleven tested) were found to have higher values. This suggests that phage
 CC bearing scFv fragments having weak affinities can be selected with
 CC antigen, probably due to the avidity of the multiple antibody heads on
 CC the phage. See also AAR21260-307, 309-311; AAR22450, 565-581
 XX

SQ Sequence 113 AA;

Alignment Scores:
 Pred. No.: 1-1e-47 Length: 113
 Score: 557.00 Matches: 108
 Percent Similarity: 89.26% Conservative: 0
 Best Local Similarity: 89.26% Mismatches: 5
 Query Match: 82.76% Indels: 8
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x AAR21268 (1-113)

QY 1 CAGGTGCAGCTGCAGGAGCTCTGGACCTGGCTGGCTGGCCCTCACAGAGCCTGTCCATC 60
 DB 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGCACCTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
 DB 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTyrPheValArgGlnPro 40
 QY 121 CCAGGAAGGCTCTGGAGCTGGCTGGCTATATGGACTGTGGAGGACACAAATATATAAT 180
 DB 41 ProGlyLysGlyLeuGlnTyrLeuGlyValIleTyrAlaGlyGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGAACAACTCCAGAGCCCAAGTTTCTTA 240
 DB 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAATGACACTCTGCAGCTGATCAGACACACCCATGTACTACTGTGCCAGAGATCGATCT 300
 DB 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
 QY 301 ACTATGATTACGGCCTATGCTATGACTACTCTGGGCGCCCAAGGACACCCGTCACCGCTCC 360
 DB 101 -----AspTyrTrpGlyGlnGlyThrThrValThrValSer 112
 QY 361 TCA 363

DB 113 Ser 113
 |||
 RESULT 2
 ADF77174
 ID ADF77174 standard; protein; 115 AA.
 XX
 AC ADF77174;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Anti-VAP-1 monoclonal antibody MoIG6 H chain.
 XX
 KW complementarity determining region; CDR; mouse;
 KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
 KW chimeric; inflammatory disorder; rheumatoid arthritis;
 KW inflammatory bowel disease; autoimmune disease; psoriasis;
 KW immunoscintigraphic imaging.
 XX
 OS Mus sp.
 XX
 FN WO2003093319-A1.
 XX
 PD 13-NOV-2003.
 XX
 PF 28-APR-2003; 2003WO-FI000330.
 XX
 PR 29-APR-2002; 2002FI-00000807.
 XX
 FA (BIOT-) BIOTIE THERAPIES CORP.
 XX
 PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;
 XX
 DR WPI; 2004-022642/02.
 XX

PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
 PT encoding nucleic acid molecules, useful for diagnosing and treating
 PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
 XX

PS Disclosure; Fig 1; 56pp; English.

CC This sequence represents a heavy chain variable region from a mouse anti-
 CC Vascular Adhesion Protein-1 (VAP-1) antibody. This sequence is included
 CC in the specification for comparison with the antibody of the invention.
 CC The murine antibody sequences of the invention may be used in the
 CC production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic
 CC acid molecules, polypeptides or antibodies are useful in treating VAP-1
 CC mediated inflammatory disorders, such as rheumatoid arthritis, The
 CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
 CC chimeric VAP-1 antibody is further used for in vitro and in vivo
 CC diagnostic applications, including in vivo immunoscintigraphic imaging of
 CC inflammation sites. The chimeric MAB's of the invention have improved
 CC kinetic properties compared to the corresponding murine antibodies.
 XX

SQ Sequence 115 AA;

Alignment Scores:
 Pred. No.: 1-76e-47 Length: 115
 Score: 555.00 Matches: 106
 Percent Similarity: 90.91% Conservative: 4
 Best Local Similarity: 87.60% Mismatches: 5
 Query Match: 82.47% Indels: 6
 DB: 8 Gaps: 1

US-10-049-868A-2 (1-363) x ADF77174 (1-115)

QY 1 CAGGTGCAGCTGCAGGAGCTCTGGACCTGGCTGGCTGGCCCTCACAGAGCCTGTCCATC 60
 DB 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGCACCTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
 DB 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTyrPheValArgGlnPro 40

QY 121 CCAGAAAGGCTGGAGTGGCTGGAGTAGTATGAGTGGTGGAGCACAATTTATAAT 180
 Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValleTrpAlaGlyGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAAAGACAACTCCAGAGCCCAAGTTTCTTA 240
 Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAATGAACAGTCTGGAGACTGATGACACAGCCCATGTACTGTGTCGAGAGATCGATCT 300
 Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAsp----- 98
 QY 301 ACTATGATTACGGCCTATGCTATGAGTACTTGGGGCCCAAGGACCCAGGTCACCGTCTCC 360
 Db 99 -----SeryTyrSerPheAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 114
 QY 361 TCA 363
 Db 115 Ser 115
 RESULT 3
 ABR44627
 ID ABR44627 standard; protein; 125 AA.
 XX
 AC ABR44627;
 XX
 DT 25-JUL-2003 (first entry)
 XX
 DE Murine variable heavy chain amino acid sequence MUVH1B.
 XX
 KW Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 KW neoplastic disorder.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 XX WO2003024388-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 30-MAY-2002; 2002WO-US017204.
 XX
 XX 20-SEP-2001; 2001US-0324100P.
 XX
 XX 08-MAR-2002; 2002US-0362612P.
 XX
 XX (CORR) CORNELL RES FOUND INC.
 XX
 XX Bander N;
 XX
 XX WPI; 2003-313319/30.
 XX
 XX Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.
 XX
 PS Disclosure; Fig 12B; 225pp; English.
 XX
 CC The present invention describes a method (M1) for ablating or killing an
 CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
 CC vascular endothelial cell proximate to the cell, with an antibody (or its
 CC antigen-binding fragment), which binds specifically to the extracellular
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
 CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,
 CC antiinflammatory and antiallergic activities, and can be used in
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by
 CC administering to the subject, an amount of an antibody which binds
 CC specifically to the extracellular domain of PSMA (the subject is a

CC mammal, preferably human and is having, or at risk of, a skin disorder).
 CC The skin disorder is a dermal or an epidermal disorder, and is selected
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
 CC vulgaris, eruptive (glutinate) psoriasis, psoriatic erythroderma,
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular
 CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosacea,
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
 CC ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis,
 CC preferably psoriasis. M1 is useful for treating a skin disorder such as
 CC an inflammatory or neoplastic disorder of the epidermis or dermis,
 CC preferably an epidermal precancerous or cancerous lesion. M1 is also
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 125 AA;

Alignment Scores:
 Pred. No.: 2.84e-47 Length: 125
 Score: 553.00 Matches: 109
 Percent Similarity: 89.60% Conservative: 3
 Best Local Similarity: 87.20% Mismatches: 9
 Query Match: 82.17% Indels: 4
 DB: 6 Gaps: 2

US-10-049-868A-2 (1-363) x ABR44627 (1-125)

QY 1 CAGGTGCAGTCGAGGAGTCTGGACTGGCTGGCTGGCGCCCTCAGAGCCCTGTCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGCACTCTCTCGGATTTCATTAAACAGATATGCTGTACAC-----TGGTTTCGC 114
 Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisValSerTrpValArg 40
 QY 115 CAGCCTCCAGAAAGGCTCTGGAGTGGCTGGGAGTAAATATGACTGCTGCAGACACAAT 174
 Db 41 GlnProGlyLysGlyLeuGluTrpLeuGlyValleTrpAlaGlyGlySerThrAsn 60
 QY 175 TATAATTCGGCTCTCATGTCCAGATCAGCATCAGCAAAAGACAACTCCAGAGCCCAAGTT 234
 Db 61 TyrAsnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysGlnVal 80
 QY 235 TTCTTAAAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTCTGTCCAGAGAT 294
 Db 81 PheLeuLysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAsp 100
 QY 295 CGATCTACTATGATTACGGCC-----TATGCTATGACTACTGGGGCCCAAGGACCCACG 348
 Db 101 ArgGlyArgTyrTyrTyrSerGlyTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSer 120
 QY 349 GTCACCGCTCTCCTCA 363
 Db 121 ValThrValSerSer 125

RESULT 4
 ABR97414

ID ABR97414 standard; protein; 667 AA.

XX

AC ABR97414,

XX

DT 30-MAY-2003 (first entry)

XX

DE Anti-human seminal plasma protein ScFv/hCPA fusion protein.

XX

KW Single chain antibody; ScFv; anti-human seminal plasma protein;

KW monoclonal antibody E8B7; mouse; murine; human; carboxypeptidase A; hCPA;

KW fusion protein; antibody-directed enzyme prodrug therapy; ADEPT;

KW methotrexate-alpha-peptide prodrug; prostate cancer; cytostatic; gene;

XX

XX

OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Protein 1..245
FT /label= E4B7 derived ScFv
FT /note= "Anti-human seminal plasma protein single chain
FT antibody derived from murine monoclonal antibody E4B7 VH
FT and VL regions; targets fusion protein to prostate cancer
FT cells"
FT 1..122
FT /note= "Corresponds to monoclonal antibody E4B7 VH (heavy
FT chain variable region"
FT 123..137
FT /label= ScFv_linker
FT 138..245
FT /note= "Corresponds to monoclonal antibody E4B7 VL (light
FT chain variable region"
FT 216
FT /note= "Encoded by GAC"
FT 245..251
FT /label= ScFv_hCPA_linker
FT Misc-difference 247
FT /note= "Encoded by AGC"
FT 253..667
FT /label= hCPA
FT /note= "Human carboxypeptidase A; activates methotrexate-
FT alpha-peptide prodrug"
XX WO2002100431-A1.
XX
XX
PD 19-DEC-2002.
XX
PF 08-JUN-2001; 2001WO-CN000924.
XX
PR 08-JUN-2001; 2001WO-CN000924.
XX
PA (UYTA-) UNIV TANGDU HOSPITAL FORTH MILITARY MEDL.
PA (HAOX/) HAO X.
XX
PI Hao X;
XX
DR WPI; 2003-156924/15.
DR N-PSDB; ABZ75116.
XX
PT Pharmaceutical kits for use in the treatment of prostate cancer, comprise
PT anti-human seminal plasma protein single-chain antibody/human
PT carboxypeptidase fusion protein and a prodrug of methotrexate-alpha-
PT peptides.
XX
PS Claim 3; Fig 4; 29pp; Chinese.
XX
CC The invention relates to a pharmaceutical kit for antibody-directed
CC enzyme prodrug therapy (ADEPT) to treat prostate cancer. The kit
CC comprises several respective containers for holding anti-human seminal
CC plasma protein single-chain antibody (ScFv)/human carboxypeptidase A
CC (hCPA) fusion protein (ABP97414), a prodrug of methotrexate-alpha-peptide
CC and a pharmaceutically-acceptable auxiliary for medication. The invention
CC also encompasses the anti-human seminal plasma protein ScFv/hCPA fusion
CC protein, and the nucleic acid encoding it (ABZ75116). This was
CC constructed by linking DNA encoding the ScFv (itself generated by linking
CC DNAs encoding the heavy and light chain variable regions (VH and VL) of
CC the murine anti-human seminal plasma protein monoclonal antibody E4B7) to
CC DNA encoding human carboxypeptidase A via a linker. The ScFv portion of
CC the fusion protein enables it to be specifically targeted to prostate
CC cancer cells, where the hCPA portion can then activate the prodrug which
CC in turn has cytostatic activity towards the cancer cells. The invention
CC permits the fusion protein to be easily produced in large quantities for
CC use in ADEPT for prostate cancer treatment. The present sequence
CC represents the ScFv/hCPA fusion protein of the invention
XX

SQ Sequence 667 AA;
Alignment Scores: 1.46e-46 Length: 667
Pred. NO.: 547.00 Matches: 105
Score: 91.74% Conservative: 6
Best Local Similarity: 86.78% Mismatches: 8
Query Match: 81.28% Indels: 2
DB: 6 Gaps: 1
US-10-049-868A-2 (1-363) x ABP97414 (1-667)
QY 1 CAGGTGACAGCTGCGAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCGCTGTCATC 60
DB 2 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnAsnLeuSerIle 21
QY 61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGTGTACACTGGGTGCGCAGCCT 120
DB 22 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 41
QY 121 CCAGGAAAGGGTCTGGAGTGGCTGGAGTAAATATGAGTGGTGGAGCACAAATATATAT 180
DB 42 ProGlyIysGlyLeuGluTrpLeuGlyValIleTrpThrGlyArgSerThrThrTyrAsn 61
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCCAGAGCGCAAGTTTCTTA 240
DB 62 SerAlaLeuMetSerArgLeuSerIleSerIysAspAsnSerGluSerGlnValPheLeu 81
QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
DB 82 LysMetAsnSerLeuGlnThrAspAspThrAlaIleTyrTyrCysGly-----ArgGly 99
QY 301 ACTATGATTACGGCTTATGCTATGGACTACTGGGCGCCAGGACCAACGTCACCGTCTCC 360
DB 100 GlyLeuIleThrSerPheAlaMetAspTyrTrpGlyGlnGlyThrThrValThrValSer 119
QY 361 TCA 363
DB 120 Ser 120
RESULT 5
ID AAU72867
XX AAU72867 standard; protein; 253 AA.
AC AAU72867;
XX
DT 26-FEB-2002 (first entry)
DE P5-9 single chain Fv.
XX
KW Human; NK2D; NK2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI10;
KW helminth; cystostatic; antimicrobial; immunomodulatory; 11B2D10; 6HYE7;
KW 8G7C10; 6ESA7; 11B2D10x4-7; 8G7C10x4-7; 6ESA7x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
OS Homo sapiens.
PN WO200171005-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-EP003414.
XX
PR 24-MAR-2000; 2000EP-00106467.
XX (KUFE/) KUFE P.
XX
PI Kufer P, Riethmueller G, Lutterbues R, Borschert K, Kischel R;

PI	Mayer M, Hofmeister R;
XX	
DR	WPI: 2002-055119/07.
DR	N-PSDE; AAS97141.
XX	
PT	Multifunctional polypeptides comprising binding sites that specifically
PT	recognize extracellular groups of the NGK2D receptor complex and domains
PT	which function as receptors or ligands, useful for treating cancers and
PT	infectious diseases.
XX	
XX	Example 7; Fig 16; 114pp; English.
PS	
CC	The invention relates to a multifunctional polypeptide comprising a
CC	domain with a binding site that specifically recognises an extracellular
CC	group of the NGK2D receptor complex and a second domain which functions
CC	as a receptor or ligand. The polypeptide and its associated
CC	polynucleotide are used for the preparation of a pharmaceutical
CC	composition for the treatment of cancer, infections and/or autoimmune
CC	conditions. The cancer may be a tumour of the head and neck, stomach,
CC	oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC	larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, chryoid
CC	bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma
CC	The infectious diseases can be caused by viruses, bacteria, fungi,
CC	protozoa or helminths. The autoimmune diseases include multiple
CC	sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC	uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC	diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC	autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NGK2D
CC	receptor and the polypeptides of the invention
XX	
SQ	Sequence 253 AA;

Alignment Scores:		
Pred. No.:	1.6e-46	Length:
Score:	\$46.00	Matches:
Percent Similarity:	90.16%	Conservative:
Best Local Similarity:	88.52%	Mismatches:
Query Match:	81.13%	4
DB:	5	Gaps:
		2
US-10-049-868A-2 (1-363) x AAU72867 (1-253)		

Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGACAGCTGCGACACTGATGACACAGCCATGTACTACTGTGGCCAGAGATCGATCT 300
Db 81 LysIleAsnSerLeuGlnThrAspThrAlaLeuTyrTyrCysAlaArgAspGlySer 100
QY 301 ACTATGATTACGGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360
Db 101 SerProTyr---TyrTyrSerMetGluTyrTrpGlyGlnGlyThrSerValThrValSer 119
QY 361 TCA 363
Db 120 Ser 120
RESULT 7
AAR32843
ID AAR32843 standard; protein; 222 AA.
XX
AC AAR32843;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1993 (first entry)
XX
DE VH NQ2/12.4-Vk NQ10/12.5 linked peptide sequences #2.
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
KW NQ2/12.4; NQ10/12.5.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..113
FT Peptide /label= VH_NQ2/12.4
FT Peptide 114..115
FT Region /note= "Linker peptide"
FT Region 116..222
FT Peptide /label= Vkappa_NQ2/12.4
XX
FN WO9303151-A1.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-GB001483.
PR 10-AUG-1991; 91GB-00017352.
PR 11-JUN-1992; 92GB-00012419.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Embleton MJ, Gorochov G, Jones PT, Winter GP;
PI WPI; 1993-076508/09.
DR N-PSDB; AAQ37462.
XX
PT Treatment of cell populations, partic. hybridomas - to link together
PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
PS Disclosure; Fig 5; 72pp; English.
XX
CC The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC and the Vk light chain genes of the antiphenyloxazolone hybridomas
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
CC cell PCR. The cDNA encoding these peptides was synthesised using forward
CC primers annealing to the Ck gene and the JH segment, followed by assembly
CC with linker primers, VH back primers based on the VH3 leader sequence and
CC a forward Ck primer nested in respect to the primer used for cDNA. The
CC assembled product within the cells is then amplified with nested primers
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC In-cell PCR may be used to determine gene linkage analysis, particularly
CC for the cloning of gene combinations that are polymorphic within a
CC population of cells, such as the rearranged genes for Ig or TCR V

CC regions. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 222 AA;
Alignment Scores:
Pred. No.: 1.02e-45 Length: 222
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1
US-10-049-868A-2 (1-363) x AAR32843 (1-222)
QY 1 CAGGTGACGCTGCGAGAGTCTGGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAACACAGATATGTGTACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTipValArgGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCTGGAGTCT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAGAGCCAACTTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCGACACTGATGACACAGCCATGTACTACTGTGGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113
RESULT 8
AAR32840
ID AAR32840 standard; protein; 235 AA.
XX
AC AAR32840;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1993 (first entry)
XX
DE VH NQ2/12.4-Vk NQ10/12.5 linked peptide sequences.
XX
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
KW NQ2/12.4; NQ10/12.5.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..113
FT Peptide /label= VH_NQ2/12.4
FT Peptide 114..127
FT Region /note= "Linker peptide"
FT Region 128..235
XX
FN WO9303151-A1.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-GB001483.

```

XX PR 10-AUG-1991; 91GB-00017352.
XX PR 11-JUN-1992; 92GB-00012419.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PI Embleton MJ, Gorochov G, Jones PT, Winter GP;
XX DR WPI; 1993-076508/09.
XX DR N-PSDB; AAQ37459.
XX PT Treatment of cell populations, partic. hybridomas - to link together
XX PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX PS Disclosure; Fig 2; 72pp; English.
XX SS
CC The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC and the VK light chain genes of the antiphenylloxazalone hybridomas
CC N02/12.4 and N010/12.5 which have been linked via a linker peptide by in-
CC cell PCR. The cDNA encoding these peptides was synthesised using forward
CC primers annealing to the CK gene and the JH segment, followed by assembly
CC with linker primers, VH back primers based on the VH3 leader sequence and
CC a forward CK primer, nested in respect to the primer used for cDNA. The
CC assembled product within the cells is then amplified with nested primers
CC annealing to the 5' end of the VH gene and the 3' end of the JK segment.
CC In-cell PCR may be used to determine gene linkage analysis, particularly
CC for the cloning of gene combinations that are polymorphic within a
CC population of cells, such as the rearranged genes for Ig or TCR V
CC regions. (Updated on 25-MAR-2003 to correct FN field.)
XX CC
XX SQ Sequence 235 AA;

Alignment Scores:
Pred. No.: 1.02e-45 Length: 235
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x AAR32840 (1-235)
QY 1 CAGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCTGTCCATC 60
DB 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
QY 61 ACTTGCACCTCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCCGACGCT 120
DB 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGCTCTGGAGTGGCTGGAGTATATGGACTGGTGGAGCACAAATTTAAT 180
DB 41 ProGlyLysGlyLeuGluTrpLeuGlyValileTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAACACAACTCCAGAGCCCAAGTTTCTTA 240
DB 61 SerAlaLeuMetSerArgLeuSerileSerlyshspasnSerlyshValPheLeu 80
QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGACTACTGTGCCAGAGATCGATCT 300
DB 81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCTATGCTATGACACTTGGGGCCAGGGACACGGTCCACGTTCC 360
DB 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
DB 113 Ala 113

RESULT 9
AAG66520
ID AAG66520 standard; protein; 142 AA.

```

```

XX AC AAG66520;
XX DT 22-OCT-2001 (first entry)
XX DE Mouse antibody 26 heavy chain variable region.
XX KW Mouse; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
XX KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
XX KW T cell; humanised antibody; autoimmune disorder; graft rejection;
XX KW allergy; antibody 26; heavy chain variable region; VH.
XX OS Mus musculus.
XX PN WO200154732-A1.
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-US002653.
XX PR 27-JAN-2000; 2000US-0178473P.
XX PA (GEMY ) GENETICS INST INC.
XX PI Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
XX PI O'hara D, Hinton P, Tsurushita N;
XX DR WPI; 2001-483195/52.
XX DR N-PSDB; AAH76438.
XX PT Novel antibody-toxic group conjugate comprising an antibody that
XX PT recognizes a molecule expressed only on activated T cells, useful for
XX PT modulating immune response for treating autoimmune disorder, allergic
XX PT response.
XX PS Example 7; Page 84; 123pp; English.
XX SS The invention relates to an antibody-toxic group conjugate comprising an
XX CC antibody that specifically recognises a molecule expressed only on
XX CC activated T cells, and a toxic group. The T cell molecule is preferably
XX CC human cytotoxic T lymphocyte associated antigen 4 (CTLA4). The antibody
XX CC of the invention is a humanised anti-CTLA4 antibody comprising a sequence
XX CC of 128 or 142 amino acids fully defined in the specification. The
XX CC antibody-toxic group conjugate is useful for modulating the immune
XX CC response in a subject suffering from a disorder or condition such as
XX CC autoimmune disorder, immune response to a graft, allergic response or an
XX CC immune response to a therapeutic protein. The antibody is also useful for
XX CC research purposes, e.g., in staining and isolating CTLA4-bearing cells.
XX CC The antibody is also useful for T-cell typing, for isolating specific IL-
XX CC 2 receptor-bearing cells or fragments of the receptor, for vaccine
XX CC preparation, and for determining the effectiveness of an agent to down-
XX CC regulate CTLA4 activity. The present sequence is the heavy chain variable
XX CC region of mouse antibody 26. It was used in the construction of the
XX CC humanised anti-CTLA4 antibody of the invention
XX SQ Sequence 142 AA;

Alignment Scores:
Pred. No.: 1.21e-45 Length: 142
Score: 537.00 Matches: 104
Percent Similarity: 89.43% Conservative: 6
Best Local Similarity: 84.55% Mismatches: 11
Query Match: 79.79% Indels: 2
DB: 4 Gaps: 1

US-10-049-868A-2 (1-363) x AAG66520 (1-142)
QY 1 CAGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCTGTCCATC 60
DB 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 39
QY 61 ACTTGCACCTCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCCGACGCT 120

```


PT tumor in individual, by administering antibody containing light and heavy
 PT chain variable region sequences contained in sequence of specified amino
 PT acids.

XX Example 2; Fig 3; 82pp; English.

PS The invention relates to the recurrence and/or development of a
 XX ganglioside GD2-associated tumour, e.g. melanoma, in an individual which
 CC is delayed by administration of an antibody comprising light and heavy
 CC chain variable region sequences of the anti-idiotypic monoclonal antibody
 CC 1A7. The antibody is used for delaying recurrence and/or development of
 CC GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or
 CC small cell lung cancer, in individual, and for treating individual with
 CC GD2-associated tumour. The present sequence is a unique peptide region
 CC from an antibody sequence resembling the anti-idiotypic antibody 1A7 heavy
 CC chain.

XX SQ Sequence 119 AA;

Alignment Scores:
 Pred. No.: 1.87e-45 Length: 119
 Score: 535.00 Matches: 104
 Percent Similarity: 88.43% Conservative: 3
 Best Local Similarity: 85.95% Mismatches: 12
 Query Match: 79.49% Indels: 2
 DB: 6 Gaps: 1

US-10-049-868A-2 (1-363) x ADA14778 (1-119)

Qy 1 CAGTGCAGCTGCAGAGCTCGACCTGGCTGGTGGCCCTCACAGAGCTGTCCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
 Qy 61 ACTTGCAGCTGTCTGGGATTTCAATAACAGATATGTTACACTGGTTCGCCAGCCT 120
 Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
 Qy 121 CCAGGAAGGCTCGGAGTGGCTGGAGTAATATGGACTGGTGAAGCACAAATATAAT 180
 Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTrpAsn 60
 Qy 181 TCGCTCTCATGTCCAGACTGAGCATCAGCAAGCAACATCCAGAGCCAAAGTTTCTTA 240
 Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 Qy 241 AAATGACAGCTGCAGACTGATGACACAGCCATGACTACTGTGCCAGAGATCGATCT 300
 Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaArgGlu***** 100
 Qy 301 ACTATGATTACGGCTATGCTATGACTACTGGGCGCAAGGACACCGGTACCGTCTCC 360
 Db 101 *****TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119
 Qy 361 TCA 363
 Db 119 Ser 119

RESULT 12

ADC35320
 ID ADC35320 standard; protein; 119 AA.

XX AC ADC35320;

XX DT 18-DEC-2003 (first entry)

XX DE Anti-idiotypic antibody VH region consensus sequence.

XX Mouse: monoclonal antibody; 1A7; anti-idiotypic antibody; ganglioside GD2;
 KW cytosolic; melanoma; neuroblastoma; small cell lung cancer; tumour;
 KW antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine.
 XX OS Synthetic.
 OS Mus sp.

XX US2003114398-A1.
 XX 19-JUN-2003.
 PD 21-MAY-2002; 2002US-00153401.

XX 17-JAN-1995; 95US-00372676.
 PR 16-JAN-1996; 96US-00591196.
 PR 15-APR-1999; 99US-00293533.
 XX (CHAT/) CHATTERJEE M.
 PA (FOON/) FOON K A.
 PA (CHAT/) CHATTERJEE S K.

XX Chatterjee M, Foon KA, Chatterjee SK;

XX WPI; 2003-810913/76.

XX Novel anti-idiotypic monoclonal antibody 1A7, that is capable of
 PT recruiting a tumor-specific response against glycosphingolipid GD2,
 PT useful for treating a GD2-associated disease e.g., melanoma, glioma, soft
 PT tissue sarcoma.

XX Example 2; SEQ ID NO 16; 84pp; English.

XX The invention relates to a monoclonal antibody 1A7 (an anti-idiotypic
 CC antibody eliciting an anti-GD2(ganglioside) response). Also included are
 CC an antibody producing cell deposited under ATCC Accession No. HB-11786
 CC (or its progeny), a polynucleotide comprising a sequence encoding a
 CC polypeptide with immunological activity of 1A7 (where the polypeptide
 CC comprises at least 5 consecutive amino acids from a variable region of
 CC 1A7), an isolated polynucleotide comprising a region of at least 20
 CC consecutive nucleotides that is capable of forming a stable duplex with a
 CC polynucleotide encoding the light or heavy chain variable region of 1A7
 CC under conditions where the region does not form a stable hybrid with a
 CC polynucleotide consisting of a variable region encoding sequence
 CC appearing as ADC35321 - ADC35370, a host cell comprising the
 CC polynucleotide, a fusion polypeptide comprising 1A7, a humanised antibody
 CC comprising 5 consecutive amino acids from the 1A7 variable regions and a
 CC vaccine comprising the antibodies. The antibodies are useful for
 CC eliciting an immune response in an individual, and for treating a GD2-
 CC associated disease in an individual. The GD2-associated diseases is
 CC chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and
 CC small cell carcinoma. The individual has a clinically detectable tumour,
 CC and the method is for palliating the GD2-associated disease. 1A7 is
 CC preferably useful for treating a tumour that was previously detected in
 CC the individual and has been treated and is clinically undetectable at the
 CC time of the administering of 1A7, or for reducing the risk of recurrence
 CC of a clinically detectable tumour. 1A7 and the humanised antibody are
 CC useful for detecting the presence of an anti-GD2 antibody bound to a
 CC tumour cell. The present sequence represents a consensus sequence for the
 CC light or heavy chain variable region of monoclonal antibody 1A7.

XX SQ Sequence 119 AA;

Alignment Scores:
 Pred. No.: 1.87e-45 Length: 119
 Score: 535.00 Matches: 104
 Percent Similarity: 88.43% Conservative: 3
 Best Local Similarity: 85.95% Mismatches: 12
 Query Match: 79.49% Indels: 2
 DB: 7 Gaps: 1

US-10-049-868A-2 (1-363) x ADC35320 (1-119)

Qy 1 CAGTGCAGCTGCAGAGCTGTGACCTGGCTGGTGGCCCTCACAGAGCTGTCCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
 Qy 61 ACTTGCAGCTGTCTGGGATTTCAATAACAGATATGTTACACTGGTTCGCCAGCCT 120
 Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAAATATGAGTGTGGTGAAGCACAAATATATAAT 180
 Db |||||
 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCATGTCAGACTGAGCATGACGAAAGACAACTCCAGAGCCAAAGTTTCTTA 240
 Db |||||
 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAAATGAACAGCTCAGACTGATGACACAGAGCCATGTACTACTGTGCCAGAGATCGATCT 300
 Db |||||
 81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgGlu***** 100
 QY 301 ACTATGATTACGGCTATGCTATGACTACTGGGCCAAGGACACAGGTACCCGTCCTCC 360
 Db |||||
 101 *****TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 118
 QY 361 TCA 363
 Db |||||
 119 Ser 119

RESULT 13

AAW07438
 ID AAW07438 standard; protein; 123 AA.

XX AC AAW07438;

XX DT 12-AUG-1997 (first entry)

XX DE Anti-DNA antibody 11f8 group heavy chain variable region.

XX KW Heavy chain; variable region; anti-DNA; monoclonal; antibody; 11f8 group;
 KW hairpin; diagnosis; inflammatory glomerulonephritis;
 KW systemic lupus erythematosus; screening; treatment; prevention; SLE;
 KW disease; consensus; putative.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Region 1..30
 FT /label= framework_I
 FT Region 31..35
 FT /label= CDR_I
 FT Region 36..49
 FT /label= framework_II
 FT Region 50..66
 FT /label= CDR_II
 FT Region 67..98
 FT /label= framework_III
 FT Region 99..112
 FT /label= CDR_III
 FT Region 113..123
 FT /label= J_region

XX WO9636361-A1.

XX PD 21-NOV-1996.

XX PF 16-MAY-1996; 96WO-US0071113.

XX PR 18-MAY-1995; 95US-00443540.

XX PA (UNMI) UNIV MICHIGAN.

XX PI Glick GD, Swanson PC;

XX DR WPI; 1997-011854/01.

XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
 PT develop prods. for diagnosis and treatment of disorders, e.g.
 PT glomerulonephritis or systemic lupus erythematosus.

PS Example; Fig 9; 102pp; English.

XX The present sequence is the heavy chain variable region of the group 11f8
 CC putative consensus anti-DNA monoclonal antibody (Mab), which has a high
 CC affinity for single stranded DNA, low or no affinity for double stranded
 CC DNA and specifically binds a DNA hairpin. The Mab can be used to diagnose
 CC disorders associated with the pathological complexation of DNA, e.g.
 CC inflammatory glomerulonephritis and systemic lupus erythematosus. It can
 CC also be used to generate reagents to screen for pharmaceutical agents,
 CC and treat and/or prevent an above disorder. The sequence was derived by
 CC aligning homologous anti-DNA Mab, whose sequences have been published, as
 CC well as several Mab of other specificities obtained from a database
 XX search

XX SQ Sequence 123 AA;

Alignment Scores:

Pred. No.: 2,38e-45 Length: 123
 Score: 534.00 Matches: 107
 Percent Similarity: 88.62% Conservative: 2
 Best Local Similarity: 86.99% Mismatches: 12
 Query Match: 79.35% Indels: 2
 DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x AAW07438 (1-123)

QY 1 CAGGTGACAGCTGCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
 Db |||||
 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGCACTGTCTCGGATTTCTATAACAGATATGTGTACACTGGGTTCGCCAGGCT 120
 Db |||||
 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
 QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAAATATGAGTGTGGTGAAGCACAAATATATA 177
 Db |||||
 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpProAlaGlyGlySerThrAsnTyr 60
 QY 178 AATTCGGCTCTCATGTCAGACTGAGCATGACGAAAGACAACTCCAGAGCCAAAGTTTTC 237
 Db |||||
 61 AsnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe 80
 QY 238 TTAATAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGA 297
 Db |||||
 81 LeuLysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgHisLeu 100
 QY 298 TCT---ACTATGATTACGGCCCTATGCTATGACTACTGGGCCAAGGACACAGCTCACC 354
 Db |||||
 101 ProTyrGlyAsnTyrGlyTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThr 120

RESULT 14

AAAR32569
 ID AAR32569 standard; protein; 269 AA.

XX AC AAR32569;

XX DT 25-MAR-2003 (revised)

XX DT 08-JUN-1993 (first entry)

XX DE Fusion protein encoded by Ox VH-hinge-VL insert.

XX KW Spacer peptide; secretable; single chain; antibody; recombinant; scAb;

XX KW rDNA; linker; Bos taurus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Region 1..22

XX FT /note= "SS"

XX FT Region 23..1135

FT /note= "VH"
 FT 136..163
 FT /note= "CBHI hinge"
 FT 164..277
 FT /note= "VL"
 XX
 FN F19103434-A.
 XX
 PD 17-JAN-1992.
 XX
 XX
 PF 16-JUL-1991; 91FI-00913434.
 XX
 XX
 PR 16-JUL-1990; 90US-00552751.
 XX
 PA (TERE-) TECH RES CENT FINLA.
 XX
 XX WPI; 1992-134225/17.
 DR N-PSDB; AAQ36982.
 DR
 XX
 PT
 PS
 PS
 CC The sequence is that of the fusion protein encoded by the Ox VH-CBHI hinge-VL insert which was used as part of a method for cloning secretable, biologically active single chain antibodies (scabs) and other secretable fusion proteins having at least 2 distinct functional proteins or domains. NOTE: This patent has been indexed using data derived from patent WO9302198-A. (First Major Country Equivalent). (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 269 AA;

Alignment Scores:
 Pred. No.: 2,65e-45 Length: 269
 Score: 534.00 Matches: 103
 Percent Similarity: 86.78% Conservative: 2
 Best Local Similarity: 85.12% Mismatches: 8
 Query Match: 79.35% Indels: 8
 DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x AAR32569 (1-269)

QY 1 CAGGTGAGCTGCAGGAGTCTGGACCTGGCTGGCTGGCGCCCTCACAGAGCTGTCATC 60
 Db 23 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 42
 QY 61 ACTTGCACTCTCTGGGATTTTCATTAAACAGATATGGTGATATGGTGGTTTCGCCAGCCT 120
 Db 43 ThrCysThrAlaSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 62
 QY 121 CCAGAAAGGGTCTGGAGTGGCTGGAGTATATGGACTGGTGGAGCAACAATTAAT 180
 Db 63 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 82
 QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTA 240
 Db 83 SerAlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 102
 QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGATCTGTCGAGAGATCGATCT 300
 Db 103 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly 122
 QY 301 ACTATGATTACGGCCTATGCTATGAGACTACTGGGGCCCAAGGACCAAGTCACGGTCTCC 360
 Db 123 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValser 134
 QY 361 TCA 363
 Db 135 Ala 135

RESULT 15
 AAB49243

ID AAB49243 standard; protein; 476 AA.
 XX
 AC AAB49243;
 XX
 DT 15-MAR-2001 (first entry)
 XX
 DE Chimeric 4H6 anti-DR4 antibody heavy chain protein.
 XX
 KW Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis; autoimmune.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200073349-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US014599.
 XX
 PR 28-MAY-1999; 99US-00322875.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;
 XX WPI; 2001-041145/05.
 DR
 XX Novel anti-death receptor 4 antibodies useful for treating cancer and immune related disorders such as rheumatoid arthritis, sjogren's syndrome, Grave's disease and diabetes mellitus.
 PT
 PT
 XX Claim 16; Fig 18; 126pp; English.
 PS
 CC The present invention relates to an anti-Death receptor 4 (DR4) antibody. The antibodies of the invention are useful for inducing apoptosis in mammalian cancer cells such as colon cancer cells and for treating an immune-related disease in a mammal such as arthritis and autoimmune disease
 CC
 XX
 SQ Sequence 476 AA;
 Alignment Scores:
 Pred. No.: 4.58e-45 Length: 476
 Score: 532.00 Matches: 102
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 80.95% Mismatches: 7
 Query Match: 79.05% Indels: 6
 DB: 4 Gaps: 1
 US-10-049-868A-2 (1-363) x AAB49243 (1-476)
 QY 4 GTGCAGCTGCAGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCTGTCATCACT 63
 Db 21 ValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerileThr 40
 QY 64 TGCATGTCTCTGGGATTTTCATTAAACAGATATGGTGATATGGTGGTTTCGCCAGCTCCA 123
 Db 41 CysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProPro 60
 QY 124 GGAAGGGTCTGCAGCTGGCTGGAGTATATGGACTGGTGGAGGCAACAATTAATTCG 183
 Db 61 GlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaValGlySerThrAsnTyrAsnSer 80
 QY 184 GCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTAAAA 243
 Db 81 AlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeuLys 100
 QY 244 ATGAACAGTCTGCAGACTGATGACACAGCCATGATCTACTGTGCCAGAGAT----- 294
 Db 101 MetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgGlnGlyGluPhe 120
 QY 295 -----CGATCTACTATGATTACGGCCTATGCTATGAGCTACTGGGGCCCAAGGACC 345

Db 121 AspTyrTyrGlySerSerLeuLeuSerTyrHisSerMetAsnPheTrpGlyGlnGlyThr 140
QY 346 ACGGTCACCGTCCTCA 363
Db 141 SerValThrValSerSer 146

Search completed: October 13, 2004, 13:21:06
Job time : 84.9571 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:28:16 ; Search time 70.3978 Seconds

(without alignments)

3328.244 Million cell updates/sec

Title: US-10-049-868A-2

Perfect score: 673

Sequence: 1 caggtgcaggtgcaggagtc.....ccacggtcacggtctctotca 363

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 2713116

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

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4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-10-803-622-218

; Sequence 218, Application US/10803622

; Publication No. US20040157214A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge Antibody Technology

; APPLICANT: Cambridge Antibody Technology Limited

; APPLICANT: Medical Research Council

; APPLICANT: McCafferty, John

; APPLICANT: Pope, Anthony

; APPLICANT: Johnson, Kevin

; APPLICANT: Hoogenboom, Hendricus

; APPLICANT: Griffiths, Andrew

; APPLICANT: Jackson, Ronald

; APPLICANT: Holliger, Kasper

; APPLICANT: Marks, James

; APPLICANT: Clackson, Timothy

; APPLICANT: Chiswell, David

; APPLICANT: Winter, Gregory

; APPLICANT: Bonert, Timothy

; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

; FILE REFERENCE: 13839-00013

; CURRENT APPLICATION NUMBER: US/10/803,622

1	557	82.8	113	16	US-10-803-622-218	Sequence 218, App
2	557	82.8	113	16	US-10-803-653-218	Sequence 218, App
3	546	81.1	253	15	US-10-239-656-63	Sequence 63, Appl
4	537	79.8	142	9	US-09-772-103-4	Sequence 4, Appl
5	535	79.5	119	14	US-10-153-401-16	Sequence 16, Appl
6	532	79.0	476	16	US-10-660-128-12	Sequence 12, Appl
7	531.5	79.0	140	8	US-08-973-518-4	Sequence 4, Appl
8	531.5	79.0	140	9	US-09-007-093-4	Sequence 4, Appl
9	531.5	79.0	140	14	US-10-428-754-4	Sequence 2, Appl
10	531	78.9	119	14	US-10-232-187-2	Sequence 23, Appl
11	526	78.2	119	15	US-10-239-656-23	Sequence 15, Appl
12	523	77.7	119	14	US-10-144-644-15	Sequence 15, Appl
13	523	77.7	119	16	US-10-700-740-15	Sequence 3, Appl
14	521.5	77.5	112	9	US-09-824-286-3	Sequence 252, App
15	521	77.4	121	14	US-10-207-655-252	Sequence 254, App
16	521	77.4	271	14	US-10-207-655-254	Sequence 254, App
17	521	77.4	556	14	US-10-207-655-268	Sequence 108, App
18	517.5	76.9	116	14	US-10-169-351-108	Sequence 187, App
19	517.5	76.9	241	16	US-10-803-622-187	Sequence 183, App
20	517.5	76.9	241	16	US-10-803-653-187	Sequence 183, App
21	517.5	76.9	272	16	US-10-803-622-183	Sequence 183, App
22	517.5	76.9	272	16	US-10-803-653-183	Sequence 183, App
23	515.5	76.6	120	14	US-10-194-975-112	Sequence 112, App
24	514.5	76.4	116	14	US-10-194-975-100	Sequence 100, App
25	510.5	75.9	135	16	US-10-351-748-31	Sequence 31, Appl
26	510.5	75.9	135	17	US-10-351-748-31	Sequence 31, Appl
27	508.5	75.6	333	14	US-10-059-261-61	Sequence 61, Appl
28	505.5	75.1	139	8	US-08-779-784-37	Sequence 37, Appl
29	505.5	75.1	241	15	US-10-353-721-13	Sequence 13, Appl
30	503	74.7	249	9	US-09-730-374-3	Sequence 3, Appl
31	503	74.7	249	16	US-10-704-206-3	Sequence 3, Appl
32	502	74.6	121	11	US-09-842-776A-52	Sequence 52, Appl
33	501.5	74.5	116	15	US-10-435-299-4	Sequence 4, Appl
34	501.5	74.5	118	14	US-10-056-052-16	Sequence 16, Appl
35	500	74.3	121	14	US-10-056-052-12	Sequence 12, Appl
36	494.5	73.5	119	13	US-10-140-555-2	Sequence 2, Appl
37	494.5	73.5	139	9	US-09-881-823-4	Sequence 4, Appl
38	493.5	73.3	120	16	US-10-697-399-5	Sequence 5, Appl
39	491.5	73.0	135	14	US-10-010-729-68	Sequence 68, Appl
40	490.5	72.9	116	16	US-10-682-845-53	Sequence 53, Appl
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42	490.5	72.9	492	16	US-10-682-845-61	Sequence 61, Appl
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44	490.5	72.9	492	16	US-10-682-845-65	Sequence 65, Appl
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; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-218

Alignment Scores:
Pred. No.: 2,05e-48 Length: 113
Score: 557.00 Matches: 108
Percent Similarity: 89.26% Conservative: 0
Best Local Similarity: 89.26% Mismatches: 5
Query Match: 82.76% Indels: 8
DB: 16 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-803-622-218 (1-113)

QY 1 CAGGTGCAGCTGCAGAGTCTGGAGCTGGCTGGCGCCCTCAGAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGACGTCTCTGGGATTTCAATAACAGATATGTGTACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGCAACAATTATAAT 180
Db 41 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCCTATGCTATGACTACTGGGCGCCAGGACACCGTCAACGCTCTCC 360
Db 101 -----AspTyrTrpGlyGlnGlyThrThrValThrValSer 112
QY 361 TCA 363
Db 113 Ser 113

RESULT 2

US-10-803-653-218
; Sequence 218, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology

; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-218
Alignment Scores:
Pred. No.: 2,05e-48 Length: 113
Score: 557.00 Matches: 108
Percent Similarity: 89.26% Conservative: 0
Best Local Similarity: 89.26% Mismatches: 5
Query Match: 82.76% Indels: 8
DB: 16 Gaps: 1
US-10-049-868A-2 (1-363) x US-10-803-653-218 (1-113)
QY 1 CAGGTGCAGCTGCAGAGTCTGGAGCTGGCTGGCGCCCTCAGAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGACGTCTCTGGGATTTCAATAACAGATATGTGTACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGCAACAATTATAAT 180
Db 41 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300

```
Db      81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaAaGAspArgGly 100
QY      301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACCAAGGTACCGTCTCC 360
Db      101 -----AspTyrTrpGlyGlnGlyThrThrValThrValSer 112
QY      361 TCA 363
Db      113 Ser 113

RESULT 3
US-10-239-656-63
; Sequence 63, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPIOTOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-3 single
US-10-239-656-63

Alignment Scores:
Pred. No.: 3,01e-47 Length: 253
Score: 546.00 Matches: 108
Percent Similarity: 90.16% Conservative: 2
Best Local Similarity: 88.52% Mismatches: 8
Query Match: 81.13% Indels: 4
DB: 15 Gaps: 2

US-10-049-868A-2 (1-363) x US-10-239-656-63 (1-253)
QY      1 CAGGTGCAG---CTGCAGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTC 57
Db      1 GluValGlnLeuLeuGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSer 20
QY      58 ATCACTGCAGTCTCTGGGATTTCATTAACAGATATGGTGTACACTGGGTTCGCCAG 117
Db      21 IleThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGln 40
QY      118 CTCCAGGAAGGCTGGAGTGGCTGGAGTAATATGACCTGGTGGAGCACAAATAT 177
Db      41 ProProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyr 60
QY      178 AATTCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTTC 237
Db      61 AnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe 80
QY      238 TTTAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGA 297
Db      81 LeuLysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArg 100
```

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QY      298 TCTACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACCAAGGTACCGTC 357
Db      101 -----TyrTyrValGlyAlaMetAspTyrTrpGlyGlnGlyThrThrValThrVal 117
QY      358 TCCTCA 363
Db      118 SerSer 119

RESULT 4
US-09-772-103-4
; Sequence 4, Application US/09772103
; Publication No. US20020039581A1
; GENERAL INFORMATION:
; APPLICANT: Carreno, Beatriz M.
; APPLICANT: Wood, Clive
; APPLICANT: Turner, Katherine
; APPLICANT: Collins, Mary
; APPLICANT: Gray, Gary S.
; APPLICANT: Morris, Donna
; APPLICANT: O'Hara, Denise
; APPLICANT: Hinton, Paul
; APPLICANT: Tsushnita, Naoya
; TITLE OF INVENTION: ANTIBODIES AGAINST CTLA4 AND USES THEREFOR
; FILE REFERENCE: GNN-009CP
; CURRENT APPLICATION NUMBER: US/09/772,103
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/178,473
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-772-103-4

Alignment Scores:
Pred. No.: 2,36e-46 Length: 142
Score: 537.00 Matches: 104
Percent Similarity: 89.43% Conservative: 6
Best Local Similarity: 84.55% Mismatches: 11
Query Match: 79.79% Indels: 2
DB: 9 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-772-103-4 (1-142)
QY      1 CAGGTGCAGTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db      20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39
QY      61 ACTTGCACTGTCTGGGATTTCATTAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
Db      40 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValTyrTrpValArgGlnPro 59
QY      121 CCAGAAAAGGCTCGAGTGGCTGGGAGTAATATGACTGGTGGAGGACCAAAATTAAT 180
Db      60 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlyThrThrAsnTyrAsn 79
QY      181 TCGGCTCTCATGTCCAGACTGAGCATCAGAAAGCAACTCCAGAGCCAAAGTTTCTTA 240
Db      80 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 99
QY      241 AAAATGAACAGTCTGCAGACTGATGACACAGCATGTACTACTGTGCCAGA-----GAT 294
Db      100 LysMetSerSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgGlyProPro 119
QY      295 CCATCTACTACTATTACGGCCCTATGCTATGCACTACTGGGGCCAAAGGACCAAGTCCACC 354
Db      120 HisAlaMetMetLysArgGlyTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValIle 139
QY      355 GTCTCCTCA 363
Db      140 ValSerSer 142
```

RESULT 5
 US-10-153-401-16
 ; Sequence 16, Application US/10153401
 ; Publication No. US20030114398A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chatterjee, Malaya
 ; Foon, Kenneth A.
 ; Chatterjee, Sunil K.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
 ; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/153,401
 ; FILING DATE: 27-Aug-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/293,533
 ; FILING DATE: 1999-04-15
 ; APPLICATION NUMBER: US 08/372,676
 ; FILING DATE: 1995-01-17
 ; APPLICATION NUMBER: US 08/591,196
 ; FILING DATE: 1996-01-16
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Catherine M. Polizzi
 ; REGISTRATION NUMBER: 40,130
 ; REFERENCE/DOCKET NUMBER: 304142000202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 119 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-10-153-401-16

Alignment Scores:
 Pred. No.: 3,718-46 Length: 119
 Score: 535.00 Matches: 104
 Percent Similarity: 88.43% Conservative: 3
 Best Local Similarity: 85.95% Mismatches: 12
 Query Match: 79.45% Indels: 2
 DB: 14 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-153-401-16 (1-119)

QY 1 CAGGTGACGTGCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCTGTGCCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGACATGCTCTGGGATTTCATTAACAGATATGTTACACTGGGTTCCGACGCT 120
 Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
 QY 121 CCAGAAAGGCTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGCACAAATATAAT 180

Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
 QY 181 TCGGCTCTCATGTCCAGACTGACATCAGCAAGAGCAACTCCAGAGCCAAAGTTTCTTA 240
 Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTCCAGAGATCCGATCT 300
 Db 81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgGlu***** 100
 QY 301 ACTATGATTACGGCCCTATGCTATGGACTACTGGGGCCAAAGGACACGGTCACCGTCTCC 360
 Db 101 *****TyrTyralaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 118
 QY 361 TCA 363
 Db 119 Ser 119

RESULT 6
 US-10-660-128-12
 ; Sequence 12, Application US/10660128
 ; Publication No. US20040120947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Dodge, Kelly
 ; APPLICANT: Kim, Kyung Jin
 ; TITLE OF INVENTION: DR4 Antibodies and Uses Thereof
 ; FILE REFERENCE: P1245RIP2B
 ; CURRENT APPLICATION NUMBER: US/10/660,128
 ; CURRENT FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US/09/584,166
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 09/322,875
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: US 09/237,299
 ; PRIOR FILING DATE: 1999-01-25
 ; PRIOR APPLICATION NUMBER: US 60/072,481
 ; NUMBER OF SEQ ID NOS: 12
 ; SEQ ID NO 12
 ; LENGTH: 476
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence is synthesized.
 ; FEATURE:
 ; NAME/KEY: Misc_feature
 ; LOCATION: 20
 ; OTHER INFORMATION: Xaa may be glutamine or glutamic acid
 US-10-660-128-12

Alignment Scores:
 Pred. No.: 8,81e-46 Length: 476
 Score: 532.00 Matches: 102
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 80.95% Mismatches: 7
 Query Match: 79.05% Indels: 6
 DB: 16 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-660-128-12 (1-476)

QY 4 GTGACGTGCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCTGTCCATCACT 63
 Db 21 ValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThr 40
 QY 64 TGCACATGCTCTGGGATTTCATTAACAGATATGTTACACTGGGTTCCGACGCTCCA 123
 Db 41 CysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60
 QY 124 GGAAGGGCTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGCACAAATATAATTCG 183
 Db 61 GlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaValGlySerThrAsnTyrAsnSer 80

Alignment Scores: 8.63e-46 Length: 140
Pred. No.: 531.50 Matches: 103
Score: 531.50 Conservative: 4
Percent Similarity: 88.43% Mismatches: 13
Best Local Similarity: 85.12% Indels: 1
Query Match: 78.97% Gaps: 1
DB: 9

US-10-049-868A-2 (1-363) x US-09-007-093-4 (1-140)

QY 1 CAGGTGACGTGACGAGTCTGGACCTGGCTGGCGCCCTCAGACGCTGTCCATC 60
Db 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40
QY 61 ACTTGACACTCTCTCGGATTTTCATTAAACAGATATGGTACACTGGGTCCCGACCT 120
Db 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60
QY 121 CCAGGAAAGGCTCGGAGTGGCTGGGAGTAATATGGACTGGTGGAGGACCAAAATTATAAT 180
Db 61 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80
QY 181 TCGGCTCTCATGTCCAGACTGACATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTA 240
Db 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPhelysSerGlnValPheLeu 100
QY 241 AAAATGAACAGTCTGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 300
Db 101 LysMetSerSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120
QY 301 ACTATGATTACGGCTATGCTATGGACTACTGGGCGCCAAAGGACCAACGGTCCCGTCC 360
Db 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139
QY 361 TCA 363
Db 140 Ser 140

RESULT 9
US-10-428-754-4
; Sequence 4, Application US/10428754
; Publication No. US2003028304A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; Barber, Brian H
; Cates, George A
; Caterini, Judith E
; Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/428,754
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 10/428,754
; FILING DATE: 05-MAY-2003
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-1065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-428-754-4

Alignment Scores: 8.63e-46 Length: 140
Score: 531.50 Matches: 103
Percent Similarity: 88.43% Conservative: 4
Best Local Similarity: 85.12% Mismatches: 13
Query Match: 78.97% Indels: 1
DB: 14 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-428-754-4 (1-140)

QY 1 CAGGTGACGTGACGAGTCTGGACCTGGCTGGCGCCCTCAGACGCTGTCCATC 60
Db 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40
QY 61 ACTTGACACTCTCTCGGATTTTCATTAAACAGATATGGTACACTGGGTCCCGACCT 120
Db 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60
QY 121 CCAGGAAAGGCTCGGAGTGGCTGGGAGTAATATGGACTGGTGGAGGACCAAAATTATAAT 180
Db 61 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80
QY 181 TCGGCTCTCATGTCCAGACTGACATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTA 240
Db 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPhelysSerGlnValPheLeu 100
QY 241 AAAATGAACAGTCTGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 300
Db 101 LysMetSerSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120
QY 301 ACTATGATTACGGCTATGCTATGGACTACTGGGCGCCAAAGGACCAACGGTCCCGTCC 360
Db 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139
QY 361 TCA 363
Db 140 Ser 140

RESULT 10
US-10-232-187-2
; Sequence 2, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830


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; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-232-187-2

Alignment Scores:
Pred. No.:          9,54e-45          Length:      119
Score:             531.00             Matches:    104
Percent Similarity: 91.74%             Conservative: 7
Best Local Similarity: 85.95%           Mismatches:  8
Query Match:       78.90%              Indels:     2
DB:                14                 Gaps:       2

US-10-049-868A-2 (1-363) x US-10-232-187-2 (1-119)
QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCTGGCTGGCGCCCTCACAGAGCTGTCCATC 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 GlnValGlnLeuLysGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGTTACACTGGTTCGCCAGCCT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 ThrCysThrValSerGlyPheSerLeu---llefTyGlyAlaHisTrpValArgGlnPro 39
QY 121 CCAGAAAGGGTCTGGAGTGGCTGGAGTAAATATGACTGGTGGGAAGCACAAATTATAAT 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 40 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyraAsn 59
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGAAAGCAACTCCAGAGCCAAAGTTTCTTA 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 SerAlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 79
QY 241 AAAATGAACAGTCTGCAGACTGATCAGACAGCATGTTACTACTGTGCGCAGAGATCATCT 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 LysIleAsnSerLeuGlnThrAspAspThrAlaLeuTyTyTyCysAlaAargaspGlySer 99
QY 301 ACTATGATTACGGCTATGCTATGACTACTGGGCGCCAGGACCAAGCAGCTACCGCTCTCC 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 100 SerProTyTyr---TyTyTySerMetGluTrpTrpGlyGlnGlyThrSerValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 11
US-10-239-656-23
; Sequence 23, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTEREUSE, RALF
; APPLICANT: LUTTEREUSE, KATRIN
; APPLICANT: BORSCHERT, ROMAN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D
; OTHER INFORMATION: Hybridoma 6H7E7 variable heavy chain
US-10-239-656-23

Alignment Scores:
Pred. No.:          3.1e-45          Length:      119
Score:             526.00             Matches:    104
Percent Similarity: 86.78%             Conservative: 1
Best Local Similarity: 85.95%           Mismatches: 14
Query Match:       78.16%              Indels:     2
DB:                15                 Gaps:       1

US-10-049-868A-2 (1-363) x US-10-239-656-23 (1-119)
QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCTGGCTGGCGCCCTCACAGAGCTGTCCATC 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerile 20
QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGTTACACTGGTTCGCCAGCCT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyGlyValHisTrpIleArgGlnPro 40
QY 121 CCAGAAAGGGTCTGGAGTGGCTGGAGTAAATATGACTGGTGGGAAGCACAAATTATAAT 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyraAsn 60
QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGAAAGCAACTCCAGAGCCAAAGTTTCTTA 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SerAlaLeuMetSerArgLeuSerileSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATCAGACAGCATGTTACTACTGTGCGCAGAGATCATCT 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 LysMetAsnSerLeuGlnIleAspAspThrAlaMetTyTyTyCysAlaA---ArgGly 98
QY 301 ACTATGATTACGGCTATGCTATGACTACTGGGCGCCAGGACCAAGCAGCTACCGCTCTCC 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 99 GlyTyGluGlyAlaAlaTrpPheGlyTyTrpGlyGlnGlyThrThrValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 12
US-10-144-644-15
; Sequence 15, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Treisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION: INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-144-644-15

Alignment Scores:
Pred. No.: 6.3e-45 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 14 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-144-644-15 (1-119)

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QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCTGGTGGCGCTTCACAGAGCCTGTCATC 60
Db 1 GlnValGlnLeuLysGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAACAGATATGCTACACATGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValargGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAATATGACCTGGTGGAGCACAAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
QY 181 TCGGCTCTCATCTCCAGACTGACATCAGCAAGACAACTCCAGAGCCAACTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATCTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaargaspProPro 100
QY 301 ACTATGATACGGCTATGCTATGACACTACTGGGCCAAGGACACCGCTCACCGTCTCC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
QY 361 TCA 363
Db 119 Ser 119
```

RESULT 13

US-10-700-740-15
Sequence 15, Application US/10700740
Publication No. US20040156850A1
GENERAL INFORMATION:

APPLICANT: Ames, Robert S.
Appelbaum, Edward R.
Chaiken, Irwin M.
Cook, Richard M.
Gross, Mitchell S.
Holmes, Stephen D.
McMillan, Lynette J.
Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-700-740-15
Alignment Scores:
Pred. No.: 6.3e-45 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 16 Gaps: 1
US-10-049-868A-2 (1-363) x US-10-700-740-15 (1-119)
QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCTGGTGGCGCTTCACAGAGCCTGTCATC 60
Db 1 GlnValGlnLeuLysGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAACAGATATGCTACACATGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValargGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGAGTAATATGACCTGGTGGAGCACAAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
QY 181 TCGGCTCTCATCTCCAGACTGACATCAGCAAGACAACTCCAGAGCCAACTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATCTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaargaspProPro 100
QY 301 ACTATGATACGGCTATGCTATGACACTACTGGGCCAAGGACACCGCTCACCGTCTCC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
 QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAACTCAGAGCCAGTTTCTTA 240
 Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
 QY 241 AAAATGAACAGTCTCAGACTGATCAGACAGCATGTACTACTGTGCCAGAGATCGATCT 300
 Db 81 LysLeuAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspProPro 100
 QY 301 ACTATTATCGGCTCTGCTATGAGTACTGGGGCCCAAGGACACACCGTCTCC 360
 Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrLeuThrValSer 118
 QY 361 TCA 363
 Db 119 Ser 119

RESULT 14

US-09-824-286-3
 ; Sequence 3, Application US/09824286
 ; Patent No. US20020028202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burkly, Linda C
 ; Benjamin, Christopher D
 ; Hession, Catherine A
 ; Whitty, Adrian
 ; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Biogen, Inc.
 ; STREET: 14 Cambridge Center
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02142
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/824,286
 ; FILING DATE: 02-Apr-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/017,466
 ; FILING DATE: 10-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kaplan, Warren A.
 ; REGISTRATION NUMBER: 34,199
 ; REFERENCE/DOCKET NUMBER: A006 PCT CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617 679-2000
 ; TELEFAX: 617 679-2838
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 112 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Alignment Scores:
 Pred. No.: 8 92e-45 Length: 112
 Score: 521.50 Matches: 98
 Percent Similarity: 92.17% Conservative: 8
 Best Local Similarity: 85.22% Mismatches: 6
 Query Match: 77.49% Indels: 3
 DB: 9 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-824-286-3 (1-112)
 QY 10 CTGAGAGAGTCTGACCTGGCTGGTGGCGCCCTCAGAGCCCTGTCCATCATTGCACT 69
 Db 1 LeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThr 20
 QY 70 GTCTCTGGATTCATTAAACAGATATGGTGTACACTGGGTTCGCCACGCTCCAGGAAG 129
 Db 21 ValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLys 40
 QY 130 GGTCTGGAGTGGCTGGGAGTAATATGGAAGTGGTGGAGCACAATAATTAAATTCGGCTCTC 189
 Db 41 GlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeu 60
 QY 190 ATGTCCAGACTGAGCATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTAAATGAAC 249
 Db 61 MetSerArgLeuAsnIleAsnArgAspAsnSerLysSerGlnIlePheLeuLysMetAsn 80
 QY 250 AGTCTGCAGACTGATCAGACAGCCATGTACTACTGTGCCAGAGATCGATCTACTATGATT 309
 Db 81 SerLeuGlnThrAspAspThrAlaIleTyrTyrCysAlaArgGluGlySerThrVal--- 99
 QY 310 ACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAACGGTCACC 354
 Db 100 -----AspSerMetAspTyrTrpGlyGlnGlyThrValThr 112

RESULT 15

US-10-207-655-252
 ; Sequence 252, Application US/10207655
 ; Publication No. US20030118592A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden-Ledbetter, Martha S.
 ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 ; FILE REFERENCE: 390069.401C1
 ; CURRENT APPLICATION NUMBER: US/10/207,655
 ; CURRENT FILING DATE: 2002-07-25
 ; NUMBER OF SEQ ID NOS: 426
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 252
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion polypeptide
 ; US-10-207-655-252

Alignment Scores:
 Pred. No.: 1 01e-44 Length: 121
 Score: 521.00 Matches: 100
 Percent Similarity: 88.43% Conservative: 7
 Best Local Similarity: 72.64% Mismatches: 14
 Query Match: 77.41% Indels: 0
 DB: 14 Gaps: 0

US-10-049-868A-2 (1-363) x US-10-207-655-252 (1-121)

QY 1 CAGGTGAGTCTGAGAGTCTGGACCTGGCTGGCGCCCTCAGAGAGCTGTCCATC 60
 Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
 QY 61 ACTTGCACTGTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
 Db 21 ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAsnTrpValArgGlnPro 40
 QY 121 CCAGAAAGGCTCTGGAGTGGCTGGAGTATATGGACTGTGTGAAGCACAAATATATAAT 180
 Db 41 ProGlyLysGlyLeuGluTrpLeuGlyWetIleTrpGlyAspGlySerThrAspTyrAsn 60
 QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAGAGCCAAAGTTTCTTA 240
 Db 61 SerAlaLeuLysSerArgLeuSerIleThrLysAspAsnSerLysSerGlnValPheLeu 80

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QY      241  AAAATGACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db      81  LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTrpCysAlaArgAspGlyTyr 100
QY      301  ACTATGATTACGGCCTTATGCTATGGACTACTGGGGCCAAAGGGACCAACGGTCAACCGTCTCC 360
Db     101  SerAsnPheHisTyrTyrValMetAspTyrTyrGlyGlnGlyThrSerValThrValSer 120
QY     361  TCA 363
Db     121  Ser 121
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Search completed: October 13, 2004, 13:53:42
Job time : 72.3878 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:48:23 ; Search time 24.2958 Seconds
(without alignments)
471.266 Million cell updates/sec

Title: US-10-049-868A-3
Perfect score: 606
Sequence: 1 DIELTQSPAINASPGKVT.....GTLKLRADAAPTIVSIFKL 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	460	75.9	235	2 S25058	Ig kappa chain - m
2	448	73.9	140	2 PL0013	Ig kappa chain pre
3	437	72.1	107	2 PC4405	Ig kappa chain v r
4	427	70.5	130	1 JL0079	Ig kappa chain pre
5	422	69.6	106	2 B54378	Ig light chain v r
6	422	69.6	107	2 A30562	Ig kappa chain v r
7	420	69.3	107	2 PD0011	Ig kappa chain v r
8	419	69.1	103	2 S29591	Ig kappa chain v r
9	419	69.1	132	2 S05268	Ig kappa chain pre
10	417	68.8	106	2 PS0071	Ig kappa chain v r
11	417	68.8	107	2 B30562	Ig kappa chain v r
12	416	68.6	106	2 G27887	Ig kappa chain v r
13	415	68.5	104	2 B49049	Ig kappa chain v r
14	413	68.2	107	2 S11113	Ig kappa chain v r
15	411	67.8	107	2 S11118	Ig kappa chain pre
16	405	66.8	107	2 S11121	Ig kappa chain v r
17	402.5	66.4	108	2 G30560	Ig kappa chain v r
18	401	66.2	107	2 PT0406	Ig kappa chain v r
19	400	66.0	107	2 PT0403	Ig light chain v r
20	399	65.8	107	2 S11112	Ig kappa chain v r
21	398	65.7	107	2 S11117	Ig kappa chain v r
22	396	65.3	107	2 PT0398	Ig light chain v r
23	394	65.0	104	2 JC6076	anti-D-dimer monoc
24	392	64.7	107	2 PT0402	Ig light chain v r
25	390	64.4	100	2 S29590	Ig kappa chain v r
26	389.5	64.3	106	2 S11114	Ig kappa chain v r
27	389	64.2	130	2 B32456	Ig kappa chain pre
28	386	63.7	107	2 PT0401	Ig light chain v r
29	385	63.5	106	2 PS0070	Ig kappa chain v r

30	385	63.5	120	2 A34871	Ig kappa chain v r
31	384	63.4	97	2 PH1084	Ig light chain v r
32	384	63.4	107	2 S11113	Ig kappa chain v r
33	384	63.4	107	2 PT0395	Ig light chain v r
34	384	63.4	130	2 S04573	Ig kappa chain pre
35	382	63.0	97	2 S26341	Ig light chain v r
36	382	63.0	107	2 S11116	Ig kappa chain v r
37	382	63.0	107	2 PT0400	Ig light chain v r
38	382	63.0	107	2 A42848	Ig light chain v r
39	380	62.7	107	2 S11123	Ig kappa chain v r
40	379	62.5	107	1 KWSX4	Ig kappa chain v r
41	376.5	62.1	145	2 PL0014	Ig kappa chain pre
42	376	62.0	105	2 S26338	Ig kappa chain v r
43	376	62.0	107	2 PT0397	Ig light chain v r
44	376	62.0	130	2 A32513	Ig kappa chain pre
45	373	61.6	120	2 S66536	Ig light chain v r

ALIGNMENTS

RESULT 1

S25058
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S25058
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A:Reference number: S25057
A:Accession: S25058
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <FIS>
A:Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 460; DB 2; Length 235;
Best Local Similarity 79.3%; Pred. No. 5.2e-33;
Matches 92; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY	2	IELTQSPAINASPGKVTMTCSASSVYVHWFQESGTFPKRIYDTSKLASVPARL 61
DB	24	IVLTQSPAINASPGKVTMTCSASSVSRKQVQKSGTSPKRWIYDTSKLASVPGRF 83
QY	62	SGSGSGTEFTLEISRVAEDVGVIYVQQLVEYPLTFGAGTKLELKRADAAPTIVSIF 117
DB	84	SGSGSGTSTSYLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRADAAPTIVSIF 139

RESULT 2

PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0013
R:Cheng, H.B.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A>Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0013
A:Molecule type: mRNA
A:Residues: 1-140 <CHE>
A:Experimental source: cell line 4C11
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:46-55/Region: complementarity-determining 1

F;71-77/Region: complementarity-determining 2
F;110-118/Region: complementarity-determining 3
F;130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 73.9%; Score 448; DB 2; Length 140;
Best Local Similarity 75.9%; Pred. No. 3.5e-32;
Matches 88; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 2 IELTQSPALMSASPGKVTMTCSASSVNMHWFQOESGTFPKRIYDTSKLASGVPARL 61
DB 24 IVLTQSPALMSASPGKVTMTCSASSVNMHWFQOQPDITSPKLIWYTSNLTASGVVPRF 83

QY 62 SSGSGSTETLTISRVAEDVGVYCCQLVEYPLTFGAGTKLELRADAAPTIVSIF 117
DB 84 SSGSGSTSYSLTISRVAEDAAATYYCQQRSSYPPTFGGKTLEMRADAPTIVSIF 139

RESULT 3
PC4405
Ig kappa chain V region (F3, anti-APP) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C;Accession: PC4405
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from human
A;Reference number: PC4405
A;Accession: PC4405
A;Molecule type: mRNA
A;Residues: 1-107 <DEN>
A;Cross-references: UNIPROT:Q8K1F0
A;Experimental source: spleen cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 437; DB 2; Length 107;
Best Local Similarity 78.5%; Pred. No. 2.5e-31;
Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIELTQSPALMSASPGKVTMTCSASSVNMHWFQOESGTFPKRIYDTSKLASGVPAR 60
DB 1 DIELTQSPALMSASPGKVTMTCSASSVNMHWFQOQKPTGSPKRIYDTSKLASGVPAR 60

QY 61 LSGSGSTETLTISRVAEDVGVYCCQLVEYPLTFGAGTKLELR 107
DB 61 FSGSGSTSYSLTISRVAEDAAATYYCQQRNDPPTFGGKTLEIKR 107

RESULT 4
JL0079
Ig kappa chain precursor V region (anti-phenylloxazolone 6F6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: JL0079; A49044; B49044
R;Kaartinen, M.; Rocca-Serra, J.; Mackelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reacting
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0079
A;Molecule type: mRNA
A;Residues: 1-130 <KAA>
A;Cross-references: GB:M27792; NID:g197159
A;Experimental source: mRNA clones for anti-phenylloxazolone antibody 6F6
A;Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A;Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R;Wilsstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A;Title: Non-random features of the repertoire expressed by the members of one V kappa gene
A;Reference number: A49044; MUID:92289826; PMID:1601044
A;Accession: A49044
A;Molecule type: DNA
A;Residues: 1-25 <MIL>
A;Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250217

A;Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A;Accession: B49044
A;Molecule type: DNA
A;Residues: 114-116 <MIL2>
A;Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
A;Experimental source: BALB/c germ-line
A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 add
A;Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
C;Genetics:
A;Gene: V(kappa)Ox1
A;Introns: 17/1
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into main disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into main disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into main disulfide bonds.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;45-109/Disulfide bonds: #status predicted

Query Match 70.5%; Score 427; DB 1; Length 130;
Best Local Similarity 78.5%; Pred. No. 2.2e-30;
Matches 84; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 2 IELTQSPALMSASPGKVTMTCSASSVNMHWFQOESGTFPKRIYDTSKLASGVPARL 61
DB 24 IVLTQSPALMSASPGKVTMTCSASSVNMHWFQOQKPTGSPKRIYDTSKLASGVPARF 83

QY 62 SSGSGSTETLTISRVAEDVGVYCCQLVEYPLTFGAGTKLELR 108
DB 84 SSGSGSTSYSLTISRVAEDAAATYYCQQRNDPPTFGGKTLEIKR 130

RESULT 5
B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B54378
R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
A;Reference number: A54378; MUID:94165109; PMID:7509814
A;Accession: B54378
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <AGA>
A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747
A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 422; DB 2; Length 106;
Best Local Similarity 78.1%; Pred. No. 4.9e-30;
Matches 82; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPALMSASPGKVTMTCSASSVNMHWFQOESGTFPKRIYDTSKLASGVPARL 61
DB 2 IVLTQSPALMSASPGKVTMTCSASSVNMHWFQOQKPTGSPKLIWYTSNLTASGVVPRF 61

QY 62 SSGSGSTETLTISRVAEDVGVYCCQLVEYPLTFGAGTKLELR 106
DB 62 SSGSGSTSYSLTISRVAEDAAATYYCQQRSSYPPTFGGKTLEIKR 106

RESULT 6
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000

```

Query Match          69.3%;   Score 420;   DB 2;   Length 107;
Best Local Similarity 76.6%;   Pred. No. 7.4e-30;
Matches 82;   Conservative 10;   Mismatches 15;   Indels 0;   Gaps 0;

Qy      1  DIELTSPTAMTSASPGKVTMTCSASSVNYMHWFOQESGTFPKRITYDTSKLASGVPAR 60
        |||
Db      1  DIELTSPTAMTSASPGKVTMTCSASSISYMHYQOKPGTSPKRWITYDTSKLASGVPAK 60
        |||

Qy      61  LSGSGSGTETLIRSRVKAEDGVVYVYQQLVEYPLTFGAGTKLELR 107
        |||
Db      61  GSGSGSGTSVLSIRVEADAATYYCQWRDNPPPTFGGGTKLEIKR 107
        |||

RESULT 8
S29591
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <AV>
A;Cross-references: EMBL:X5904; NID:g52227; PIDN:CAA41820.1; PID:g52228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>

```

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 417; DB 2; Length 106;
Best Local Similarity 78.1%; Pred. No. 1.3e-29;
Matches 82; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRRIYDTSKLASGVPARL 61
DB 2 IVLTQSPAIMSASPGKVTMTCSASSVSYMHYQKSGTSPKRWIYDTSKLASGVPARF 61
QY 62 SSGSGGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELK 106
DB 62 SGRSGTSLTSSMEADAATYYCQWSSNPNVTFGAPTLELK 106

RESULT 11

B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30562
R: Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: B30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 417; DB 2; Length 107;
Best Local Similarity 75.5%; Pred. No. 1.4e-29;
Matches 80; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRRIYDTSKLASGVPARL 61
DB 2 IVLTQSPAIMSASPGKVTMTCSASSVSYMHYQKSGTSPKRWIYDTSKLASGVPTRF 61
QY 62 SSGSGGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELR 107
DB 62 SGRSGTSLTSSMEADAATYYCQWSSNPNVTFGGTKLEIKR 107

RESULT 12

G27887
Ig kappa chain V region (H18-S415) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: G27887
R: Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a dominant self-antigen
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: G27887
A:Molecule type: DNA
A:Residues: 1-106 <CAT>
A:Cross-references: UNIPROT:Q9VDD0
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H1N1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 416; DB 2; Length 106;
Best Local Similarity 76.2%; Pred. No. 1.6e-29;
Matches 80; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRRIYDTSKLASGVPARL 61
DB 2 IVLTQSPAIMSASPGKVTMTCSASSISYMHYQKPGTSPKRWIYDTSKLASGVPTRF 61

QY 62 SSGSGGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELK 106
DB 62 SGRSGTSLTSSMEADAATYYCQWSSNPNVTFGAGTKLELK 106

RESULT 13

B49049
Ig kappa chain V region (anti-idiotypic) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49049
R: Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A:Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen-binding site
A:Reference number: A49049; MUID:93049629; PMID:1425914
A:Accession: B49049
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-104 <ARM>
A:Experimental source: BALB/c
A:Note: sequence extracted from NCBI backbone (NCBI:118298, NCBI:118299)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 415; DB 2; Length 104;
Best Local Similarity 78.6%; Pred. No. 2e-29;
Matches 81; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRRIYDTSKLASGVPARL 61
DB 2 IVLTQSPAIMSASPGKVTMTCSASSVSYMHYQKSGTSPKRWIYDTSKLASGVPARF 61
QY 62 SSGSGGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLE 104
DB 62 SGRSGTSLTSSMEADAATYYCQWSSNPNVTFGAGTKLE 104

RESULT 14

S1119
Ig kappa chain V region (clone NQ6-8.3.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S1119
R: Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolin
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S1119
A:Molecule type: mRNA
A:Residues: 1-107 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 413; DB 2; Length 107;
Best Local Similarity 76.4%; Pred. No. 3e-29;
Matches 81; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRRIYDTSKLASGVPARL 61
DB 2 IVLTQSPAIMSASPGKVTMTCSASSVSYMHYQKSGTSPKRWIYDTSKLASGVPARF 61
QY 62 SSGSGGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELR 107
DB 62 SGRSGTSLTSSMEADAATYYCQWSSNPNVTFGAGTKLELR 107

RESULT 15

S1118
Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000

C:Accession: S1118
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S1118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <KAA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 411; DB 2; Length 107;
Best Local Similarity 77.4%; Pred. No. 4.5e-29;
Matches 82; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 2 IELTSPAIMSASPGKVTMTCSASSVNYMHWFQESGTFPKRIYDTSKLASGVPARL 61
Db 2 IYLTQSPAIMSASPGKVTMTCSASSVSYMHYQQKSGTSPKRWIYDTSKLDGVPARF 61

QY 62 SGSGSGTEFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELKR 107
Db 62 SGSGSGTSYSLTISMFREDATYYCQWSSNPLTFGAGTKLXLKR 107

Search completed: October 13, 2004, 13:00:06
Job time : 26.2958 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:47:33 ; Search time 119 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-10-049-868A-3

Perfect score: 606

Sequence: 1 DIELTQSPAIMSAPGKVT.....CTKLELKRADAAPTQVSIKFL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	74.6	112	2	Q8K1F2
2	451	74.4	235	2	Q91W12
3	444	73.3	134	2	Q8VDD0
4	433	71.5	112	2	Q8K1F0
5	421	69.5	107	1	KV6F MOUSE
6	419	69.1	112	2	Q8K1F3
7	419	69.1	114	2	Q8K1F1
8	416	68.6	107	1	KV6I MOUSE
9	415	68.5	107	1	KV6H MOUSE
10	415	68.5	235	2	Q7TMK0
11	414	68.3	107	1	KV6G MOUSE
12	411	67.8	111	2	AAR10981
13	411	67.8	111	2	AAR10982
14	411	67.8	111	2	AAR10994
15	410	67.7	108	2	AAR11048
16	409	67.5	110	2	AAR10999
17	408	67.3	107	1	KV6J MOUSE
18	398	65.7	107	2	AAR11015
19	392	64.7	106	2	Q9U410
20	386	63.7	108	1	KV6K MOUSE
21	385	63.5	107	1	KV6C MOUSE
22	380	62.7	107	1	KV6B MOUSE
23	379.5	62.6	214	2	Q9R1A5
24	379	62.5	107	1	KV6A MOUSE
25	379	62.5	107	1	KV6D MOUSE
26	377	62.2	111	2	AAR11009
27	374	61.7	106	2	AAR11006
28	373.5	61.6	235	2	Q7TS98
29	370	61.1	107	1	KV6E MOUSE
30	368.5	60.8	131	2	Q811C3
31	366	60.4	97	2	AAR11055

32	364	60.1	92	2	AAR11066
33	364	60.1	95	2	AAR11062
34	360.5	59.5	114	2	AAR10983
35	358.5	59.2	234	2	Q8R062
36	358	59.1	111	2	AAR11021
37	356.5	58.8	234	2	Q8VCP0
38	355.5	58.7	237	2	Q7SZ36
39	354	58.4	129	1	KV4A MOUSE
40	353.5	58.3	236	2	Q7Z3Y4
41	350.5	57.8	112	2	AAR11019
42	347.5	57.3	114	2	AAR11022
43	347.5	57.3	236	2	Q6PIH7
44	347.5	57.3	236	2	Q6GMX9
45	347.5	57.3	236	2	AAR34141
					AAR11066 mus muscu
					AAR11062 mus muscu
					AAR10983 mus muscu
					Q8R062 mus muscu
					AAR11021 mus muscu
					Q8VCP0 mus muscu
					Q7SZ36 xenopus lae
					P01680 mus muscu
					Q7Z3Y4 homo sapien
					AAR11019 mus muscu
					AAR11022 mus muscu
					Q6PIH7 homo sapien
					Q6GMX9 homo sapien
					AAR34141 homo sapi

ALIGNMENTS

```

RESULT 1
Q8K1F2
ID Q8K1F2 PRELIMINARY; PRT; 112 AA.
AC Q8K1F2;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Pianque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516283; AAM64201.1; --
DR PIR; H33932; H33932.
DR HSSP; Q91W12; IAY1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;

Query Match 74.6%; Score 452; DB 2; Length 112;
Best Local Similarity 78.6%; Pred. No. 5.5e-38;
Matches 88; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMSAPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLASGVPAR 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIVLTQSPAIMSAPGKVTITCNASSSVNYMHWFQOESGTFPKRRIYDTSKLASGVPAR 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 61 LSGSGSGTFTLISRVKADGVVYQQLVPLTFGAGTKLELKRADAAP 112
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 FSGSGSGTSTLISRVKADGVVYQQLVPLTFGAGTKLELKRADAAP 112
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PDB; 1AY1; X-ray; L=23-232.
DR PDB; 1HQ4; X-ray; A/C=23-235.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBDE58FEF CRC64;

Query Match 74.4%; Score 451; DB 2; Length 235;
Best Local Similarity 76.7%; Pred. No. 1.6e-37;
Matches 89; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 2 ILTQSPAIMSASPGKVTMTCSASSVNMHWFOQESGTFPKRIYDTSKLASGVPARL 61
Db 24 IVLTQSPAIMSASPGKVTMTCSASSVNMHWYQKSGTSPKRWIYDTSKLVGPD 83

QY 62 SSGSGSTFTLEISRVKAEDGVVYCOQLVEYPLTFGAGTKLEKRAADAAPT 117
Db 84 SSGSGSTSYSLTISNMEAEADVATYCCQWSRNPTTFGVGKLEKRAADAAPT 139

RESULT 3
Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name-anti-MOG kappa;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

Query Match 71.5%; Score 433; DB 2; Length 112;
Best Local Similarity 77.1%; Pred. No. 4.7e-36;
Matches 84; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSVNMHWFOQESGTFPKRIYDTSKLASGVPARL 63
Db 4 LTQSPAIMSASPGKVTMTCSASSVNMHWYQKSGTSPKRWIYDTSKLASGVPAR 63

QY 64 SSGSGSTFTLEISRVKAEDGVVYCOQLVEYPLTFGAGTKLEKRAADAAPT 112
Db 84 SSGSGSTSYSLTISNMEAEADVATYCCQWSRNPTTFGVGKLEKRAADAAPT 139
[1]
```

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RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RC Semi P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RC Chernaiovsy Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR PIR; G27887; G27887.
DR HSSP; P01834; 1MIM.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR NON TER 134
FT NON TER 134
SQ SEQUENCE 134 AA; 14525 MW; CDFDF8E2236E2D0CF CRC64;

Query Match 73.3%; Score 444; DB 2; Length 134;
Best Local Similarity 76.6%; Pred. No. 4.4e-37;
Matches 85; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 2 ILTQSPAIMSASPGKVTMTCSASSVNMHWFOQESGTFPKRIYDTSKLASGVPARL 61
Db 24 IVLTQSPAIMSASPGKVTMTCSASSVNMHWYQKSGTSPKRWIYDTSKLASGVPAR 83

QY 62 SSGSGSTFTLEISRVKAEDGVVYCOQLVEYPLTFGAGTKLEKRAADAAPT 112
Db 84 SSGSGSTSYSLTISNMEAEADVATYCCQWSRNPTTFGVGKLEKRAADAAPT 134

RESULT 4
Q8K1F0 PRELIMINARY; PRT; 112 AA.
AC Q8K1F0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

Query Match 71.5%; Score 433; DB 2; Length 112;
Best Local Similarity 77.1%; Pred. No. 4.7e-36;
Matches 84; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSVNMHWFOQESGTFPKRIYDTSKLASGVPARL 63
Db 4 LTQSPAIMSASPGKVTMTCSASSVNMHWYQKSGTSPKRWIYDTSKLASGVPAR 63

QY 64 SSGSGSTFTLEISRVKAEDGVVYCOQLVEYPLTFGAGTKLEKRAADAAPT 112
Db 84 SSGSGSTSYSLTISNMEAEADVATYCCQWSRNPTTFGVGKLEKRAADAAPT 139
[1]
```


RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kertanen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gricham J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055911; AAH5911.1; -;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25861 MW; 3EBA0312A87613F4 CRC64;

Query Match 68.5%; Score 415; DB 2; Length 235;
Best Local Similarity 72.8%; Pred. No. 7.4e-34;
Matches 83; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

Oy 4 LTQSPALMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRIYDTSKLASGVPARLSG 63
Db 26 LTQSPALMSASLGKVTMTCSASSSVNYMHWFQESGTFPKRIYDTSKLASGVPARLSG 85

Oy 64 SGSGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLEKRAADAAPTVSIF 117
Db 86 SGSGTSYSLTISVVEADAATYCCQQLSTSPWTFGGGSKLEIKRAADAAPTVSIF 139

RESULT 11
KV6G MOUSE
ID _KV6G_MOUSE STANDARD; PRT; 107 AA.
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGF response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00737; AAA38682.1; -;
DR HSSP; Q91W12; IAY1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 68.3%; Score 414; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 3.8e-34;
Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Oy 2 IELTQSPALMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRIYDTSKLASGVPARL 61
Db 2 ILLTQSPALMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRIYDTSKLASGVPARF 61

Oy 62 SGSGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLEKLR 107
Db 62 SGSGTSYSLTISVVEADAATYCCQQLSTSPWTFGGGSKLEIKRAADAAPT 111

RESULT 12
AAR10981
ID AAR10981 PRELIMINARY; PRT; 111 AA.
AC AAR10981;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436821; AAR10981.1; -;
DR NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11819 MW; EE2F666368BC91BC CRC64;

Query Match 67.8%; Score 411; DB 2; Length 111;
Best Local Similarity 71.8%; Pred. No. 7.9e-34;
Matches 79; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Oy 4 LTQSPALMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRIYDTSKLASGVPARLSG 63
Db 2 MTQTPILSASPGKVTMTCSASSSVNYMHWFQESGTFPKRIYDTSKLASGVPARFSG 61

Oy 64 SGSGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLEKRAADAAPT 113
Db 62 SGSGTSYSLTISVVEADAATYCCQQLSTSPWTFGGGSKLEIKRAADAAPT 111

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RESULT 13
AAR10982 PRELIMINARY; PRT; 111 AA.
AC AAR10982;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436822; AAR10982.1; -.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 11819 MW; EE2F666368BC91BC CRC64;

Query Match 67.8%; Score 411; DB 2; Length 111;
Best Local Similarity 71.8%; Pred. No. 7.9e-34;
Matches 79; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSSVNVMHWFOQESGTFPKRIYDTSKLAGVPAFLSG 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 MTQTPTILSASPGKVTMTCRASSSVNVMHWFOQKPGSPKWIYATSNLAGVPAFLSG 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 SSGSGTEFTLEISRVAEDVGYYCOQLVEYPLTFGAGTKLELKRADAAPT 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGTSYSLTISRMEADAATYYCQWSSNPPTFGGKTKLEIKRADAAPT 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
AAR10994 PRELIMINARY; PRT; 111 AA.
AC AAR10994;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436834; AAR10994.1; -.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 11914 MW; 69E94859D33DAGBF CRC64;

Query Match 67.8%; Score 411; DB 2; Length 111;
Best Local Similarity 70.0%; Pred. No. 7.9e-34;
Matches 77; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSSVNVMHWFOQESGTFPKRIYDTSKLAGVPAFLSG 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 MTQTPTAIMSASGSGKVTMTCSASSSVNVMHWFOQKPGSPRLIYDTSNLAGVPIRFTG 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 SSGSGTEFTLEISRVAEDVGYYCOQLVEYPLTFGAGTKLELKRADAAPT 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGTSYSLTISRMEADAATYYCQWSSYPLTVGTGKLELKRADAAPT 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
AAR11048 PRELIMINARY; PRT; 108 AA.
AC AAR11048;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436888; AAR11048.1; -.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C11222F2FDFBC160 CRC64;

Query Match 67.7%; Score 410; DB 2; Length 108;
Best Local Similarity 72.0%; Pred. No. 9.7e-34;
Matches 77; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSSVNVMHWFOQESGTFPKRIYDTSKLAGVPAFLSG 63
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Db 1 MTQTPTAIMSASGKVTMTCSASSSVNVMHWFOQKPGSPRLIYDTSNLAGVPPVRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 SSGSGTEFTLEISRVAEDVGYYCOQLVEYPLTFGAGTKLELKRADA 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SSGSGTSYSLTISRMEADAATYYCQWSSYPWTFGGTKLEIKRADA 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: October 13, 2004, 12:59:11
Job time : 120 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:44:23 ; Search time 111.067 Seconds
(without alignments)
384.353 Million cell updates/sec

Title: US-10-049-868A-3
Perfect score: 606
Sequence: 1 DIELTQSPAIMASPGKVT.....GFKLEKRAAPTIVSIFKL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	77.7	215	7 ADE06764	Adm06764 D18 light
2	466	76.9	144	8 ADM79827	Adm79827 Mouse Igg
3	460	75.9	135	2 AAR08347	Aar08347 Light cha
4	459	75.7	129	5 ABB75616	Abb75616 Anti-RANK
5	458	75.6	235	2 AAW41392	Aaw41392 Chimeric
6	452	74.6	108	2 AAR21301	Aar21301 Murine VL
7	452	74.6	156	8 ADO43520	Ado43520 Amino aci
8	451	74.4	215	2 AAR43674	Aar43674 Mouse ant
9	451	74.4	215	2 AAR99644	Aar99644 Anti-BGH
10	451	74.4	215	2 AAR97377	Aar97377 Murine an
11	448	73.9	108	2 AAR21293	Aar21293 Murine VL
12	445	73.4	235	2 AAR13060	Aar13060 Monoclonal
13	444	73.3	241	6 ABR62010	Abr62010 Single-ch
14	444	73.3	255	3 AAB11398	Aab11398 E. coli e
15	444	73.3	255	4 AAB74199	Aab74199 PelB-scfv
16	444	73.3	255	4 AAB70769	Aab70769 Expressio
17	444	73.3	255	4 AAY72020	Aay72020 E. caroto
18	443.5	73.2	214	2 AAW15933	Aaw15933 Antibody
19	443	73.1	118	6 AAE37758	Aae37758 Murine TI
20	443	73.1	118	6 AAE37807	Aae37807 Murine TI
21	441	72.8	316	2 AAY32086	Aay32086 Single ch
22	439	72.4	108	2 AAR21303	Aar21303 Murine VL
23	439	72.4	108	2 AAW41388	Aaw41388 Anti-CEA
24	439	72.4	266	8 ADH77307	Adh77307 Yeast kil
25	439	72.4	309	4 AAB70841	Aab70841 SNV-env 1

26	437	72.1	236	2 AAY34096	Aay34096 Partial a
27	437	72.1	241	2 ABB76197	Abb76197 Anti-meso
28	437	72.1	241	4 AAB50019	Aab50019 Antimesot
29	437	72.1	288	2 AAW82482	Aaw82482 Mouse bis
30	437	72.1	539	3 AAY50823	Aay50823 Fv-antibo
31	437	72.1	554	3 AAY50822	Aay50822 Fv-antibo
32	437	72.1	562	6 ABR57059	Abr57059 Plasmid p
33	436	71.9	109	6 ABU63531	Abu63531 Anti-cucu
34	435	71.8	108	2 AAR21294	Aar21294 Murine VL
35	435	71.8	108	2 AAR21292	Aar21292 Murine VL
36	435	71.8	330	4 AAB70842	Aab70842 SNV-env 1
37	434.5	71.7	208	2 AAY44175	Aay44175 Mab Fab13
38	433	71.5	108	2 AAR79884	Aar79884 Anti-EGFR
39	433	71.5	108	3 AAB12461	Aab12461 Igg monoc
40	433	71.5	241	5 AAM48925	Aam48925 scFv anti
41	432	71.3	108	3 AAY97236	Aay97236 Variable
42	432	71.3	108	4 AAB82710	Aab82710 VEGF anta
43	432	71.3	108	5 AAE25956	Aae25956 Mouse ant
44	432	71.3	108	5 AAW74413	Aaw74413 Antigen-b
45	432	71.3	108	6 ABE26725	Abj26725 VEGF bind

ALIGNMENTS

RESULT 1
ADE06764

ID ADE06764 standard; protein; 215 AA.

AC ADE06764;

DT 29-JAN-2004 (first entry)

XX D18 light chain protein SEQ ID NO:34.

XX hybrid polypeptide; protein aggregation; prion polypeptide;
neuroprotective; nootropic; antidiabetic; anticonvulsant;
cerebroprotective; antiparkinsonian; cyostatic; nephrotropic; cardiant;
antiinflammatory; antiarteriosclerotic; gene therapy;
Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
Alzheimer's disease; Type II diabetes; Huntington's disease;
immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
familial amyloidotic polyneuropathy; medullary carcinoma;
chronic renal failure; congestive heart failure; chronic inflammation;
atherosclerosis.

OS Synthetic.

XX WO2003085086-A2.

XX 16-OCT-2003.

XX 08-APR-2003; 2003WO-USO10856.

XX 09-APR-2002; 2002US-0371610P.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Williamson RA, Moroncini G;

XX WPI; 2003-877028/81.

XX N-PSDB; ADE06763.

XX New motif-grafted hybrid polypeptides binding to the infectious form of a
prion, useful for diagnosing or treating diseases of protein aggregation
or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
diabetes.

XX Disclosure; SEQ ID NO 34; 115pp; English.

XX The present invention describes a hybrid polypeptide (I) comprising: (a)

XX DE Light chain variable region of the BMA-031 Mab.
 XX KW Human alpha/beta T-cell receptor; TCR; cancer; autoimmune disease.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..22
 XX FT Active-site /label= Signal peptide
 XX FT /label= CDR 1
 XX FT Active-site 46..55
 XX FT /label= CDR 2
 XX FT Active-site 71..77
 XX FT /label= CDR 3
 XX FT Active-site 110..118
 XX EP403156-A.
 XX 19-DEC-1990.
 XX 07-JUN-1990; 90EP-00306178.
 XX PF 07-JUN-1989; 89US-00362549.
 XX PR 25-MAY-1990; 90US-00529979.
 XX (GENZ) GENZYME CORP.
 XX PA (BEHW) BEHRINGERWERKE AG.
 XX PI Kurrie R, Shearman CW, Moore GP, Seiler F;
 XX WPI; 1990-377880/51.
 XX DR N-PSDB; AAQ06956, AAQ06958.
 XX PT Anti-human alpha-beta T-cell receptor monoclonal antibodies - used for
 XX PT immunosuppressive therapy in transplantation and as therapeutic agent for
 XX PT immuno-regulation, e.g. to treat cancer.
 XX FS Disclosure; Table 1B; 44pp; English.
 XX CC The Mab recognises the epitope on alpha/beta TCR and includes a mediator
 XX CC response. It is highly effective in clinical application before, after and
 XX CC during bone marrow transplant surgery, in treatment of cancer and
 XX CC autoimmune diseases, and has applications in immunoregulation. Abs may
 XX CC also be used in detection of immunocompetent T-cells. (Updated on 25-MAR-
 XX CC 2003 to correct PA field.)
 XX SQ Sequence 135 AA;
 Query Match 75.9%; Score 460; DB 2; Length 135;
 Best Local Similarity 80.4%; Pred. No. 1.3e-28;
 Matches 90; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 QY 2 IELTQSPAIMSASGPEKVTMTCSASSSVNMYHWFQESGTFPKRRIYDTSKLAGVAPARL 61
 Db IELTQSPAIMSASGPEKVTMTCSASSSVNMYHWFQESGTFPKRRIYDTSKLAGVAPARL 61
 QY 62 SGSSGGTFTLEISRVKAEADVGVYCOOLVEYPLTFGAGTKLEIKRADAPT 113
 Db SGSSGGTFTLEISRVKAEADVGVYCOOLVEYPLTFGAGTKLEIKRADAPT 113
 QY 84 SGSSGGTFTLEISRVKAEADVGVYCOOLVEYPLTFGAGTKLEIKRADAPT 135
 Db SGSSGGTFTLEISRVKAEADVGVYCOOLVEYPLTFGAGTKLEIKRADAPT 135
 RESULT 4
 ABB75616
 ID ABB75616 standard; protein; 129 AA.
 AC ABB75616;
 XX 10-JUN-2002 (first entry)
 XX Anti-RANK ligand mab 19H22 light chain variable region.
 XX RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;

KW complementarity determining region; CDR; rheumatoid arthritis;
 KW osteoporosis; bone cancer; metastasis; osteolysis; osteoarthritis;
 KW psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;
 KW cytostatic; antiarthritic; antiinflammatory; osteopathic; antidiabetic;
 KW antirheumatic; immunosuppressive; antipsoriatic; neuroprotective;
 KW light chain; VL; mouse.
 XX Mus musculus.
 XX OS
 XX FH Key Location/Qualifiers
 XX FT Region 24..33
 XX FT /label= CDR1
 XX FT /note= "complementarity determining region 1"
 XX FT Region 49..55
 XX FT /label= CDR2
 XX FT /note= "complementarity determining region 2"
 XX FT Region 88..96
 XX FT /label= CDR3
 XX FT /note= "complementarity determining region 3"
 XX WO200215846-A2.
 XX 28-FEB-2002.
 XX 21-AUG-2001; 2001WO-US026161.
 XX 21-AUG-2000; 2000US-0226524P.
 XX PR 07-SEP-2000; 2000US-0230639P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Sweet RW, Tornetta MA, Truneh A, Wattam TA;
 XX WPI; 2002-242022/29.
 XX DR N-PSDB; ABL53530.
 XX PT A mouse monoclonal antibody 19H22 for treating or preventing osteopenic
 XX PT disease including rheumatoid arthritis and osteoporosis.
 XX FS Claim 6; Page 7; 45pp; English.
 XX CC The present sequence is that of the light chain variable region of
 XX CC claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)
 XX CC 19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells
 XX CC obtained by immunising CB6 f1 mice with human RANK-L protein, and fusing
 XX CC spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for
 XX CC human RANK-L, having a binding affinity characterised by a dissociation
 XX CC constant of about 10 power -10 M. RANK-L is a member of the tumour
 XX CC necrosis factor family of proteins and a key regulator of the immune
 XX CC system, bone development and homeostasis. The invention provides altered,
 XX CC chimeric and humanised 19H22 antibodies, including Fab or F(ab')2
 XX CC fragments, antibodies comprising the light and heavy chain variable
 XX CC regions of 19H22, and antibodies comprising the complementarity
 XX CC determining regions of 19H22. These are used in methods for the
 XX CC diagnosis, treatment and prevention of osteopenic diseases, including
 XX CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,
 XX CC wear debris induced osteolysis or osteoarthritis, and immune diseases
 XX CC including psoriasis, insulin dependent diabetes, inflammatory bowel
 XX CC disease or multiple sclerosis. Methods are also provided for the
 XX CC recombinant production of the antibodies, using isolated nucleic acids
 XX CC and transfected host (preferably mammalian) host cells, and a method of
 XX CC diagnosing conditions associated with Th1 T-cell activity or osteoclast
 XX CC development and activation, in particular those listed above
 XX SQ Sequence 129 AA;
 Query Match 75.7%; Score 459; DB 5; Length 129;
 Best Local Similarity 76.7%; Pred. No. 1.4e-28;
 Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
 QY 2 IELTQSPAIMSASGPEKVTMTCSASSSVNMYHWFQESGTFPKRRIYDTSKLAGVAPARL 61
 IELTQSPAIMSASGPEKVTMTCSASSSVNMYHWFQESGTFPKRRIYDTSKLAGVAPARL 61

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Db      2  IVLTSQPAIMASGPEKVTMTCSASSSVYMWYQQKPGSPRLIIYDTSNLSAGVPVRF 61
QY      62  SGSGSGTFTLISRVKAEADVGYCQQLVEYPLTFGAGTKLELRADAAPTVSIF 117
        ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      62  SGSGSGTSYSLTISRMEADAATYTCQQWSNFPFLTFGAGTKLELRADAAPTVSIF 117

RESULT 5
ID      AAW41392
XX      AAW41392 standard; protein; 235 AA.
AC      AAW41392;
XX
XX      17-OCT-2003 (revised)
DT      02-JUN-1998 (first entry)
XX
XX      Chimeric anti-CEA antibody 806.077 light chain.
DE
DE      Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW      cancer diagnosis; complementarity determining region; light chain.
XX
XX      Homo sapiens.
OS
OS      Mus sp.
OS      Chimeric.
XX
XX      WO9742329-A1.
PN
XX
XX      13-NOV-1997.
PD
XX
XX      29-APR-1997; 97WO-GB001165.
PF
XX
XX      04-MAY-1996; 96GB-00009405.
PR
XX      14-FEB-1997; 97GB-00003103.
PR
XX
XX      (ZENE ) ZENECA LTD.
PA
XX
XX      Copley CG, Edge MD, Emery SC;
PI
XX
XX      WPI; 1997-558987/51.
DR
XX      N-PSDB; AAV17288.
DR
XX
XX      Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
PT      and therapy of cancer.
XX
XX      Example 8; Page 100-101; 208pp; English.
XX
XX      This sequence is the light chain variable region of the antibody of the
CC      invention. The antibody is an anti-CEA (carcinoembryonic antigen)
CC      antibody (806.077 Ab). Host cells or transgenic organisms transformed
CC      with DNA encoding the antibody, are used to make the antibody or
CC      conjugate. The conjugate is used in a medicament suitable for intravenous
CC      administration. The conjugate can be used for cancer therapy, selectively
CC      killing tumour cells. The antibody can be used for in vivo or in vitro
CC      diagnosis of cancer. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX      Sequence 235 AA;
SQ
Query Match 75.6%; Score 458; DB 2; Length 235;
Best Local Similarity 76.9%; Pred. No. 3.1e-28;
Matches 90; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY      1  DIELTQSPAIMSAPGKVTMTCSASSSVYMWYQQKPGSPRLIIYDTSNLSAGVPEAR 60
Db      23  DIELTQSPAIMSAPGKVTMTCSASSSVYMWYQQKPGSPRLIIYDTSNLSAGVPEAR 82
QY      61  LSGSGSGTFTLISRVKAEADVGYCQQLVEYPLTFGAGTKLELRADAAPTVSIF 117
Db      83  FSGSGSGTSYSLTISRMEADAATYTCQQWSNFPFLTFGAGTKLELRADAAPTVSIF 139

RESULT 6
ID      AAR21301
XX      AAR21301 standard; protein; 108 AA.

```

```

XX      AAR21301;
AC
XX      21-MAY-1992 (first entry)
DT
XX      Murine VL kappa group IV/VI chain p specific for phOx.
DE
XX      Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW      g3p; binding; adsorption; gene VIII; diverse repertoire;
XX      specific binding pairs; replicable genetic display package.
XX      Synthetic.
XX
XX      Key Location/Qualifiers
FH      Binding-site 24..33
FT      /label= CDR1
FT      Binding-site 49..55
FT      /label= CDR2
FT      Binding-site 98..96
FT      /label= CDR3
FT      /note= " D-X-G-X-X motif "
XX
XX      WO9201047-A.
PN
XX
XX      23-JAN-1992.
PD
XX
XX      10-JUL-1990; 90GB-00015198.
PF
XX
XX      10-JUL-1990; 90GB-00015198.
PR
XX      19-OCT-1990; 90GB-00022845.
PR
XX      12-NOV-1990; 90GB-00024503.
PR
XX      06-MAR-1991; 91GB-00004744.
PR
XX      15-MAY-1991; 91GB-00010549.
PR
XX
XX      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA      (MEDI-) MED RES COUNCIL.
PA
XX
XX      McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI      Jackson RH, Holliger KP, Marks JD;
XX
XX      WPI; 1992-056862/07.
DR
XX
XX      Producing members of specific binding pairs - by expression in
PT      recombinant host cells with a secreting replicable genetic display
PT      package.
XX
XX      Example 22; Fig 24; 209pp; English.
XX
XX      The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
CC      Fv library. The library produces a diverse repertoire of antibody
CC      fragments specific for 2-phenyl-5-oxazolone (phOx). It was prepd. using
CC      cDNA generated from mRNA from mice immunised with phOx coupled to chicked
CC      serum albumin. The VH and VL kappa sequences were separately amplified by
CC      PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
CC      the phage surface as fusions with gene III. The resulting library of
CC      clones was diverse; 23 hapten binding clones were sequenced revealing 8
CC      VH genes (A-H; AAR21264-71) in a variety of pairings with 7 Vκ genes (A-G
CC      ; AAR21286-92). Most clones were VH-B combinations so a further
CC      hierarchical library was prepd. by "crossing" VH-B with the Vκ
CC      repertoire. The resulting library was screened for hapten binding and 24
CC      clones sequenced. 14 new partners (AAR21293-308) for VH-B were
CC      identified. Nearly all the Vκ genes were "ox-like"; only f, (from the
CC      original library) and h, p, q, and r (from the hierarchical library) were
CC      Vκox1 type genes. Of the 24 hierarchical clones, 2 were of type "p". The
CC      kd of VH-B/Vκ-d for phox-GABA was 10 nM, one of the highest values found.
CC      This suggests that phage bearing scfv fragments having weak affinities
CC      can be selected with antigen, probably due to the avidity of the multiple
CC      antibody heads on the phage. The different combinations could also be
CC      isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
CC      AAR22450, 565-581
XX
XX      Sequence 108 AA;
SQ

```

QY	61	LSGSGSGTEFTLEISRKAEDGVVYYCQQLVEYPLTFGAGTKLELRADAAPTVSIF	117
		: : : : : : : : : : : :	
Db	61	PSGSGSGTISYSLTISSMEADAAIYYCQWSSNPFTFGSGTKLEIKRADAAPTVSIF	117
		: : : : : : : : : : : :	
 RESULT 8 AAR43674			
ID	AAR43674	standard; protein; 215 AA.	
XX	AAR43674;		
XX			
DT	25-MAR-2003	(revised)	
DT	23-MAY-1994	(first entry)	
XX			
DE	Mouse anti-bovine growth hormone MAB light chain.		
XX			
KW	Monoclonal antibody; Mab; affinity; binding; antigen; diagnostics;		
KW	therapy; imaging; purification; biosensors.		
XX			
OS	Mus musculus.		
XX			
PN	US5260203-A.		
XX			
PD	09-NOV-1993.		
XX			
PF	25-APR-1990; 90US-00512910.		
PR	02-SEP-1986; 86US-00902971.		
PR	02-SEP-1987; 87US-00092110.		
PR	19-JAN-1989; 89US-00299617.		
XX			
PA	(ENZO-) ENZON LABS INC.		
PI	Ladner RC, Bird RE, Hardman K;		
XX			
DR	WPI; 1993-367875/46.		
DR	N-PSDB; AAQ51535.		
XX			
PT	Single chain poly:peptide for binding antigen - comprising light and		
PT	heavy chain antigen binding portions linked by peptide linker.		
XX			
PS	Disclosure; Fig 22; 78pp; English.		
XX			
CC	This sequence is the mature light chain of a monoclonal antibody (Mab)		
CC	and is the starting material for the production of a single chain		
CC	polypeptide having binding affinity for a given antigen (Bovine growth		
CC	hormone). The polypeptide comprises a first polypeptide comprising the		
CC	antigen binding portion of the light chain variable region of an		
CC	antibody and a second polypeptide comprising the antigen binding portio		
CC	of the heavy chain variable region of an antibody and at least one		
CC	peptide linker linking the first and second polypeptide chains. The		
CC	resulting single chain polypeptide can be used in diagnostics, therapy		
CC	(in vivo and in vitro), imaging, purifications and biosensors. (Updated		
CC	on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct		
CC	PA field.)		
XX			
SQ	Sequence 215 AA;		
 Query Match 74.4%; Score 451; DB 2; Length 215; Best Local Similarity 78.4%; Pred. No. 1e-27; Matches 91; Conservative 6; Mismatches 17; Indels 2; Gaps			
QY	4	LTQSPAINMASPGEKVTMTCSASSV--NYMHWFQESGTFPKRIYTSTKLASGPVARL	6
		: : : : : : : : : : : :	
Db	4	LTQSPAINMASPGEKVTMTCRASSSVSSSYLLHMFQQKSGASPRLMIYSTSLASGPVARF	6
		: : : : : : : : : : : :	
QY	62	SGSGSGTEFTLEISRKAEDGVVYYCQQLVEYPLTFGAGTKLELRADAAPTVSIF	117
		: : : : : : : : : : : :	
Db	64	SGSGSGTISYLTISSVEADAAIYYCQYSGYPLTFGAGTKLELRADAAPTVSIF	119
		: : : : : : : : : : : :	
 RESULT 9 AAR99644			

ID AAR99644 standard; protein; 215 AA.
 XX AC AAR99644;
 XX
 DT 25-MAR-2003 (revised)
 DT 11-OCT-1996 (first entry)
 XX
 XX Anti-bGH monoclonal antibody light chain.
 DE
 XX Antibody engineering; single polypeptide chain binding molecule;
 KW heavy chain; light chain; monoclonal antibody; MAb;
 KW bovine growth hormone; bGH; immunoaffinity purification.
 XX
 OS Mus sp.
 XX US5534621-A.
 PN
 XX 09-JUL-1996.
 PD
 XX 06-JUN-1995; 95US-00468992.
 PF
 XX 02-SEP-1986; 86US-00902971.
 PR 02-SEP-1987; 87US-00092110.
 PR 19-JAN-1989; 89US-00299617.
 PR 25-APR-1990; 90US-00512910.
 PR 01-APR-1993; 93US-00040440.
 XX (ENZO-) ENZON LABS INC.
 PA
 XX Bird RE, Ladner RC, Hardman K;
 PI WPI; 1996-333309/33.
 XX N-PSDB; AAT13734.
 DR
 XX Immuno:purificn. using single binding chain molecule including antigen-
 PT binding parts of antibody light and heavy chain variable regions
 PT connected by a linker - is smaller, stabler and less expensive than
 PT complete antibodies.
 XX
 PS Example; Fig 22; 78pp; English.
 XX
 CC The mature heavy chain (AAR99643) and mature light chain (AAR99644) of
 CC the mouse anti-bovine growth hormone monoclonal antibody 3C2 can be
 CC utilised in novel single chain binding molecules (AAR99645-48), in which
 CC the hypervariable regions from IGG1 3C2 MAb are joined by peptide linkers
 CC derived from the Fv regions of an IGA class anti-phosphorylcholine
 CC myeloma antibody, MCP-603. The single chain molecules retain the binding
 CC specificity of the light and heavy chains and have the advantages of
 CC smaller size, greater stability and reduced cost. They can be used in
 CC therapy, diagnostics, imaging, purification and biosensors. (Updated on
 CC 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 215 AA;
 Query Match 74.4%; Score 451; DB 2; Length 215;
 Best Local Similarity 78.4%; Pred. No. 1e-27;
 Matches 91; Conservative 6; Mismatches 17; Indels 2; Gaps 1;
 QY 4 LTQSPALMSASPGKVTMTCSASSV--NYMHFQESGTFPKRIYDTSKLASGVPARL 61
 DB 4 LTQSPALMSASPGKVTMTCSASSVSSSYLHWFOQKSGASPKLWIYSTNLSASGVPARF 63
 QY 62 SSGSGSTEPTLTSIRKAEADVGVYCCQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
 DB 64 SSGSGTSYSLTSSVEADAATYYCQYSGYPLTFGAGTKLELKRADAAPTVSIF 119
 RESULT 10
 AAR97377
 ID AAR97377 standard; protein; 215 AA.
 XX
 AC AAR97377;
 XX

DT 25-MAR-2003 (revised)
 DT 13-NOV-1996 (first entry)
 XX
 DE Murine anti-BGH MAB light chain.
 XX
 XX Antibody engineering; monoclonal antibody; MAB; light chain;
 KW single chain antibody; immunoassay; bovine growth hormone; BGH.
 KW
 OS Mus musculus.
 XX US5518889-A.
 PN
 XX 21-MAY-1996.
 PD
 XX 06-JUN-1995; 95US-00468988.
 PF
 XX 02-SEP-1986; 86US-00902971.
 PR 02-SEP-1987; 87US-00092110.
 PR 19-JAN-1989; 89US-00299617.
 PR 25-APR-1990; 90US-00512910.
 PR 01-APR-1993; 93US-00040440.
 XX (ENZO-) ENZON LABS INC.
 PA
 XX Bird RE, Ladner RC, Hardman K;
 PI WPI; 1996-259060/26.
 XX N-PSDB; AAT29057.
 DR
 XX Immunoassay using single chain antigen binding mol. - as replacement for
 PT labelled or immobilised antibody, are less immunogenic, easier to
 PT engineer, more stable and less expensive.
 XX
 PS Example 1; Fig 22; 78pp; English.
 XX
 CC Portions of the heavy chain (AAR97376) and light chain (AAR97377) of
 CC murine IGG1 anti-bovine growth hormone monoclonal antibody 3C2 can be
 CC incorporated into novel single polypeptide chain binding molecules (see
 CC also AAW02188-90). These are expressed in host cells using DNA constructs
 CC (see also AAT36460-62) that include heavy and light chain encoding
 CC sequences (AAT29056 and AAT29057) joined by linker moieties. Following
 CC expression and refolding, the single chain binding molecules show the
 CC binding characteristics of the aggregate of the 2 original heavy and
 CC light chains of the variable region of the antibody. (Updated on 25-MAR-
 CC 2003 to correct PF field.)
 XX
 SQ Sequence 215 AA;
 Query Match 74.4%; Score 451; DB 2; Length 215;
 Best Local Similarity 78.4%; Pred. No. 1e-27;
 Matches 91; Conservative 6; Mismatches 17; Indels 2; Gaps 1;
 QY 4 LTQSPALMSASPGKVTMTCSASSV--NYMHFQESGTFPKRIYDTSKLASGVPARL 61
 DB 4 LTQSPALMSASPGKVTMTCSASSVSSSYLHWFOQKSGASPKLWIYSTNLSASGVPARF 63
 QY 62 SSGSGSTEPTLTSIRKAEADVGVYCCQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
 DB 64 SSGSGTSYSLTSSVEADAATYYCQYSGYPLTFGAGTKLELKRADAAPTVSIF 119
 RESULT 11
 AAR21293
 ID AAR21293 standard; protein; 108 AA.
 XX
 AC AAR21293;
 XX
 DT 21-MAY-1992 (first entry)
 DT
 DE Murine VL kappa group IV/VI chain h specific for pHox.
 XX
 XX Pd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;


```

AC ABR62010;
XX
DT 03-OCT-2003 (first entry)
XX
DE Single-chain (scFv) antibody.
XX
KW Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy;
KW antisense therapy; scFv; antibody.
XX
OS Synthetic.
XX
PN EPI321524-A1.
XX
PD 25-JUN-2003.
XX
PF 19-DEC-2001; 2001EP-00130319.
XX
PR 19-DEC-2001; 2001EP-00130319.
XX
PA (DUEB/) DUERING K.
XX
PI Mahn A, Hantke S, Petsch D;
XX
DR WPI; 2003-543829/52.
DR N-PSDB; ACC84876.
XX
XX Increasing the content of transgene-coded biomolecules in a plant or
PT animal, useful for producing proteins for diagnosing, preventing and/or
PT treating viral diseases and cancer, comprises changing the distribution
PT of ATP and/or ADP.
XX
PS Example 2; Fig 2; 18pp; English.
XX
CC The invention relates to increasing the content of one or more transgene-
CC coded biomolecules in an organism and involves changing the distribution
CC of ATP and/or ADP in cells of the organism. The yield of transgenic
CC molecules in host cells is often insufficient for industrial production.
CC The method increases the yield of transgenic molecules in animal and
CC plant host cells, therefore facilitating their production on an
CC industrial scale. The proteins produced by the method are useful for
CC diagnosing, preventing and/or treating viral diseases and cancer. The
CC present sequence represents a single-chain (scFv) antibody, used to
CC exemplify the increase in the expression of scFv antibodies in transgenic
CC potato tubers
XX
SQ Sequence 241 AA;
Query Match 73.3%; Score 444; DB 6; Length 241;
Best Local Similarity 80.0%; Pred. No. 4e-27;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMGASPGKVTMTCSASSSVYNNHWFQESGTPPKRIYDTSKLASGVPAR 60
Db 132 DIELTQSPAIMGASPGKVTMTCSASSSVYNNHWFQKSGTSPKRWIYDTSKLSGVPAR 191
QY 61 LSGSGSGTFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELRADA 110
Db 192 FSGSGSGTSYSLTSSMEAEADAATYICQWSSNPLTFGAGTKLELRADA 241

RESULT 14
AAB11398
ID AAB11398 standard; protein; 255 AA.
XX
AC AAB11398;
XX
DT 22-FEB-2001 (first entry)
XX
DE E. coli expression plasmid pUBS20-ScFvOx encoded protein.
XX
KW Eukaryotic protein; protease; interferon; antibody; hormone;
KW disulfide bridge.
XX

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OS Escherichia coli.
OS Synthetic.
XX
PN EPI048732-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-1999; 99EP-00107412.
XX
PR 26-APR-1999; 99EP-00107412.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
DR WPI; 2000-674185/66.
DR N-PSDB; AAC66074.
XX
XX Preparation of water-soluble eukaryotic polypeptides with disulfide
PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
PT presence of arginine or amide compound.
XX
PS Example 6; Page 22-23; 40pp; German.
XX
CC This invention describes a novel preparation of a water-soluble,
CC naturally occurring eukaryotic polypeptide containing two or more
CC cysteine units bound via a disulfide bridge which comprises cultivation
CC of prokaryotic cells in the presence of arginine or an amide compound.
CC The method is useful for the preparation of eukaryotic proteins e.g.
CC proteases, interferons, protein hormones, antibodies or antibody
CC fragments (e.g. a single chain FV fragment that binds to thyroid
CC stimulating hormone). It is especially useful for preparing proteins with
CC more than five disulfide bridges, e.g. recombinant plasminogen activator
CC (rPA). The technique is simple and does not require in vitro after-
CC treatment, such as the removal of inclusion bodies, reduction or
CC naturation
XX
SQ Sequence 255 AA;
Query Match 73.3%; Score 444; DB 3; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.2e-27;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMGASPGKVTMTCSASSSVYNNHWFQESGTPPKRIYDTSKLASGVPAR 60
Db 132 DIELTQSPAIMGASPGKVTMTCSASSSVYNNHWFQKSGTSPKRWIYDTSKLSGVPAR 191
QY 61 LSGSGSGTFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELRADA 110
Db 192 FSGSGSGTSYSLTSSMEAEADAATYICQWSSNPLTFGAGTKLELRADA 241

RESULT 15
AAB74199
ID AAB74199 standard; protein; 255 AA.
XX
AC AAB74199;
XX
DT 29-MAY-2001 (first entry)
XX
DE PelB-scFvOxazolone fusion protein.
XX
KW Molecular chaperone; PelB signal sequence; scFvOxazolone.
XX
OS Unidentified.
XX
PN EPI077262-A1.
XX
PD 21-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00115839.
XX
PR 29-JUL-1999; 99EP-00114811.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.

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XX  Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
PI
XX
XX  WPI: 2001-246712/26.
DR
DR  N-PSDB; AAF77806.
XX
PT  Producing naturally folded eukaryotic proteins e.g. antibodies,
PT  interferon, hormones or proteases that contain two or several cysteines
PT  linked by disulfide bridges comprises co-expression of a molecular
PT  chaperone.
XX
XX  Disclosure; Page 19; 35pp; English.
XX
XX  The present invention relates to a method for production of a naturally
CC  folded eukaryotic protein containing two or more cysteines linked by
CC  disulfide bridges. The method comprises co-expression and secretion into
CC  the periplasm of a molecular chaperone via an expression vector coding
CC  for the chaperone. The expression vector also encodes a signal sequence.
CC  The method is useful for producing a naturally folded eukaryotic protein
CC  such as an antibody, antibody fragment, interferon, protein hormone or a
CC  protease containing two or several cysteines linked by disulfide bridges.
CC  The present sequence is a fusion protein composed of the PelB signal
CC  sequence and ScFvOxazolon. This sequence was used in the method of the
CC  present invention
XX
XX  Sequence 255 AA;
SQ
Query Match          73.3%; Score 444; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.2e-27;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy  1 DIELTQSPAIMSASPEGEKVTMTCSASSSVNVMHWFQESGTFPKRIYDTSKLAGVPEAR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  132 DIELTQSPAIMSASPEGEKVTMTCSASSSVRYMWNWFQKSGTSPKRWIYDTSKLSGVPEAR 191
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy  61 LSGSGSGTEFTLEISRVAEDVGVYCOOLVEYPLTFGAGTKLELKRAA 110
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  192 FSGSGSGTSGLTITSSMEAEADATVYCOQWSSNPLTFGAGTKLELKRAA 241
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: October 13, 2004, 12:55:08
 Job time : 115.067 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:59:19 ; Search time 85,7792 Seconds
(without alignments)
447.653 Million cell updates/sec

Title: US-10-049-868A-3

Perfect score: 606

Sequence: 1 DIELTQSPAIMSAPGKVT.....GTLKLEKRAADAPTIVSIFKL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT PUB PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	77.7	215	14	US-10-410-907A-34
2	459	75.7	129	14	Sequence 34, Appli
3	459	75.7	129	16	Sequence 2, Appli
4	458	75.6	235	9	Sequence 2, Appli
5	452	74.6	108	16	Sequence 17, Appli
6	452	74.6	108	16	Sequence 251, App
7	448	73.9	108	16	Sequence 251, App
8	448	73.9	108	16	Sequence 251, App
9	446	73.6	108	16	Sequence 243, App
10	446	73.6	108	16	Sequence 243, App
11	445	73.4	235	10	Sequence 241, App
12	445	73.4	235	15	Sequence 5, Appli
13	445	73.4	235	15	Sequence 5, Appli
14	440	72.6	107	9	Sequence 5, Appli

15	440	72.6	107	9	US-09-144-886-83	Sequence 83, Appli
16	439	72.4	108	9	US-09-910-059-9	Sequence 9, Appli
17	439	72.4	108	16	US-10-803-622-253	Sequence 253, App
18	439	72.4	108	16	US-10-803-653-253	Sequence 253, App
19	436	71.9	108	16	US-10-803-622-242	Sequence 242, App
20	436	71.9	108	16	US-10-803-653-242	Sequence 242, App
21	432	71.3	107	16	US-10-632-706-79	Sequence 79, Appl
22	432	71.3	107	16	US-10-632-706-80	Sequence 80, Appl
23	432	71.3	108	9	US-09-976-787-8	Sequence 8, Appli
24	432	71.3	108	9	US-09-865-198-8	Sequence 8, Appli
25	432	71.3	240	9	US-09-976-787-28	Sequence 28, Appl
26	432	71.3	240	9	US-09-865-198-27	Sequence 27, Appl
27	432	71.3	669	9	US-09-807-721-2	Sequence 2, Appli
28	428	70.6	108	16	US-10-803-622-240	Sequence 240, App
29	428	70.6	108	16	US-10-803-653-240	Sequence 240, App
30	427	70.5	108	16	US-10-803-622-252	Sequence 252, App
31	427	70.5	108	16	US-10-803-653-252	Sequence 252, App
32	427	70.5	110	16	US-10-803-622-256	Sequence 256, App
33	427	70.5	110	16	US-10-803-653-256	Sequence 256, App
34	427	70.5	256	14	US-10-247-488-2	Sequence 2, Appli
35	427	70.5	258	14	US-10-247-488-4	Sequence 4, Appli
36	425	70.1	108	16	US-10-803-622-244	Sequence 244, App
37	425	70.1	108	16	US-10-803-653-244	Sequence 244, App
38	424	70.0	110	16	US-10-803-622-255	Sequence 255, App
39	424	70.0	110	16	US-10-803-653-255	Sequence 255, App
40	424	70.0	119	9	US-09-808-037-28	Sequence 28, Appl
41	424	70.0	119	14	US-10-162-889-28	Sequence 28, Appl
42	424	70.0	119	15	US-10-384-788-28	Sequence 28, Appl
43	424	70.0	119	15	US-10-618-856-26	Sequence 26, Appl
44	424	70.0	239	9	US-09-808-037-6	Sequence 6, Appli
45	424	70.0	239	14	US-10-162-889-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-410-907A-34
; Sequence 34, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Glanluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; FILE OF INVENTION: US05 THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Light Chain
US-10-410-907A-34

Query Match 77.7%; Score 471; DB 14; Length 215;
Best Local Similarity 77.8%; Pred. No. 7.3e-36;
Matches 91; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSAPGKVTMTCSASSSYNMHWFOESGTFPKRIYDTSKLAGVAPR 60

Db 3 ELVLTQSPAFMSAPGKVTMTCSASSSYNMHWYQKSGTSPKRIYDTSKLAGVAPR 62

QY 61 LSGSGSGTFTTLEISRVKAEADVGYCQQLVEVFLTFAGTKLEKRAADAPTIVSIF 117

Db 63 FSGSGSGTYSLTISISMEAEADATYTCQWSSNPYTFGGTKLEIKRAADAPTIVSIF 119

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US-10-344-779-2
; Sequence 2, Application US/10344779
; Publication No. US20030211106A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
; FILE REFERENCE: GP50033
; CURRENT APPLICATION NUMBER: US/10/344,779
; CURRENT FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-344-779-2

Query Match      75.7%; Score 459; DB 14; Length 129;
Best Local Similarity 76.7%; Pred. No. 5.4e-35;
Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY  2 IELTQSPAIMSASPEKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLASGVPARL 61
Db  2 IVLTQSPAIMSASPEKVTMTCSASSSVSYMYWYQKPGSPRLIIYDTSNLASGVPRF 61

QY  62 SGSGSGTEFTLEISRKAEDVGYYCOOLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db  62 SGSGSGTSYSLTISRMEADAATYYCQWSNFFLTFGAGTKLELKRADAAPTVSIF 117

RESULT 3
US-10-738-809-2
; Sequence 2, Application US/10738809
; Publication No. US20040171117A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
; FILE REFERENCE: GP50033
; CURRENT APPLICATION NUMBER: US/10/738,809
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-738-809-2

Query Match      75.7%; Score 459; DB 16; Length 129;
Best Local Similarity 76.7%; Pred. No. 5.4e-35;
Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY  2 IELTQSPAIMSASPEKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLASGVPARL 61
Db  2 IVLTQSPAIMSASPEKVTMTCSASSSVSYMYWYQKPGSPRLIIYDTSNLASGVPRF 61

QY  62 SGSGSGTEFTLEISRKAEDVGYYCOOLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db  62 SGSGSGTSYSLTISRMEADAATYYCQWSNFFLTFGAGTKLELKRADAAPTVSIF 117

RESULT 4
US-09-910-059-17
; Sequence 17, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric light chain sequence
US-09-910-059-17

Query Match      75.6%; Score 458; DB 9; Length 235;
Best Local Similarity 76.9%; Pred. No. 1.3e-34;
Matches 90; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY  1 DIELTQSPAIMSASPEKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLASGVPAR 60
Db  23 DIELTQSPAIMSASPEKVTMTCSASSSVYMYWYQKPGTFPKLWIYDTSNLASGVPAR 82

QY  61 LSGSGSGTEFTLEISRKAEDVGYYCOOLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db  83 FSGSGSGTSYSLTISRMEADAATYYCQORSTYPLTFGAGTKLEIKETVAAPSVFIF 139

RESULT 5
US-10-803-622-251
; Sequence 251, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
US-10-803-622-251

Query Match      75.6%; Score 458; DB 9; Length 235;
Best Local Similarity 76.9%; Pred. No. 1.3e-34;
Matches 90; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY  1 DIELTQSPAIMSASPEKVTMTCSASSSVNVMHWFQOESGTFPKRRIYDTSKLASGVPAR 60
Db  23 DIELTQSPAIMSASPEKVTMTCSASSSVYMYWYQKPGTFPKLWIYDTSNLASGVPAR 82

QY  61 LSGSGSGTEFTLEISRKAEDVGYYCOOLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db  83 FSGSGSGTSYSLTISRMEADAATYYCQORSTYPLTFGAGTKLEIKETVAAPSVFIF 139
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APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,622
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 251
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-251

Query Match 74.6%; Score 452; DB 16; Length 108;
Best Local Similarity 81.5%; Pred. No. 2e-34;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
Qy 1 DIETQSPALMSASPGKVTMTCSASSSVNVMHFQESGTFPKRRIYDTSKLAGVPAR 60
Db 1 DIETQSPALMSASPGKVTMTCSASSSVNVMHFQESGTFPKRRIYDTSKLAGVPAR 60
Qy 61 LSGSGSGTEFTLEISRVAEDVGVYCOQLVEYPLTFGAGTKLEKRA 108
Db 61 FSGSGSGTSYSLTSSMEAEADVATYYCQWSSNPLTFGAGTKLEKRA 108

RESULT 6
US-10-803-653-251
Sequence 251, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6

PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 251
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-251

Query Match 74.6%; Score 452; DB 16; Length 108;
Best Local Similarity 81.5%; Pred. No. 2e-34;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
Qy 1 DIETQSPALMSASPGKVTMTCSASSSVNVMHFQESGTFPKRRIYDTSKLAGVPAR 60
Db 1 DIETQSPALMSASPGKVTMTCSASSSVNVMHFQESGTFPKRRIYDTSKLAGVPAR 60
Qy 61 LSGSGSGTEFTLEISRVAEDVGVYCOQLVEYPLTFGAGTKLEKRA 108
Db 61 FSGSGSGTSYSLTSSMEAEADVATYYCQWSSNPLTFGAGTKLEKRA 108

RESULT 7
US-10-803-622-243
Sequence 243, Application US/10803622
Publication No. US20040157214A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,622
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9

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; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-243
Query Match 73.9%; Score 448; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 4.7e-34;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
;
QY 1 DIELTQSPAIMSASGEGKVTMTCSASSSVNMYHWFQBSGTPPKRIYDTSKLAGVVPAR 60
Db 1 DIELTQSPAIMSASGEGKVTMTCSASSSVNMYHWFQBSGTPPKRIYDTSKLAGVVPAR 60
;
QY 61 LSGSGSGTEFTLEISRKAEDVGVVYCOQLVEYPLTFGAGTKLEIKRA 108
Db 61 FSGSGSGTSYSLTSSMEADAATYVCQWSSNPLTFGAGTKLEIKRA 108
;
RESULT 8
US-10-803-653-243
; Sequence 243, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-241
Query Match 73.9%; Score 448; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 4.7e-34;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
;
QY 1 DIELTQSPAIMSASGEGKVTMTCSASSSVNMYHWFQBSGTPPKRIYDTSKLAGVVPAR 60
Db 1 DIELTQSPAIMSASGEGKVTMTCSASSSVNMYHWFQBSGTPPKRIYDTSKLAGVVPAR 60
;
QY 61 LSGSGSGTEFTLEISRKAEDVGVVYCOQLVEYPLTFGAGTKLEIKRA 108
Db 61 FSGSGSGTSYSLTSSMEADAATYVCQWSSNPLTFGAGTKLEIKRA 108
;
RESULT 9
US-10-803-622-241
; Sequence 241, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-243
Query Match 73.9%; Score 448; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 4.7e-34;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
;
QY 1 DIELTQSPAIMSASGEGKVTMTCSASSSVNMYHWFQBSGTPPKRIYDTSKLAGVVPAR 60
Db 1 DIELTQSPAIMSASGEGKVTMTCSASSSVNMYHWFQBSGTPPKRIYDTSKLAGVVPAR 60
;
QY 61 LSGSGSGTEFTLEISRKAEDVGVVYCOQLVEYPLTFGAGTKLEIKRA 108
Db 61 FSGSGSGTSYSLTSSMEADAATYVCQWSSNPLTFGAGTKLEIKRA 108
;
RESULT 8
US-10-803-653-243
; Sequence 243, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
```

OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-241

Query Match 73.6%; Score 446; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 7.2e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSAPGKVTMTCSASSSVNVMHWFOQSGTTPKRIYDTSKLASGVDPAR 60
DB 1 DIETQSPAIMSAPGKVTMTCSASSSVNVMHWFOQSGTTPKRIYDTSKLASGVDPAR 60
QY 61 LSGSGSGTEFTLEISRVKAEDVGVVYCOOLVEYPLTFGAGTKLELKRA 108
DB 61 FSGSGSGTSYSLTISMEADAATYCCQFSSNPLTFGAGTKLELKRA 108

RESULT 10

US-10-803-653-241
; Sequence 241, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 241
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-241

Query Match 73.6%; Score 446; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 7.2e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSAPGKVTMTCSASSSVNVMHWFOQSGTTPKRIYDTSKLASGVDPAR 60

DB 1 DIETQSPAIMSAPGKVTMTCSASSSVNVMHWFOQSGTTPKRIYDTSKLASGVDPAR 60
QY 61 LSGSGSGTEFTLEISRVKAEDVGVVYCOOLVEYPLTFGAGTKLELKRA 108
DB 61 FSGSGSGTSYSLTISMEADAATYCCQFSSNPLTFGAGTKLELKRA 108

RESULT 11

US-09-795-515-5
; Sequence 5, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-795-515-5

Query Match 73.4%; Score 445; DB 10; Length 235;
Best Local Similarity 75.0%; Pred. No. 2.1e-33;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSAPGKVTMTCSASSSVNVMHWFOQSGTTPKRIYDTSKLASGVDPARL 61
DB 24 IVLTSQSPAIMSAPGKVTMTCSASSSVNVMHWFOQSGTTPKRIYDTSKLASGVDPAHF 83
QY 62 SGSGSGTEFTLEISRVKAEDVGVVYCOOLVEYPLTFGAGTKLELKRAAAPTYSIF 117
DB 84 RSGSGSGTSYSLTISMEADAATYCCQWSSNFTFGSGTKLEINRADTAPTYSIF 139

RESULT 12

US-10-704-352-5
; Sequence 5, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.

TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-704-352-5

Query Match 73.4%; Score 445; DB 15; Length 235;
Best Local Similarity 75.0%; Pred. No. 2.1e-33;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRIYDTSKLASGVPAEL 61
DB 24 IVLTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRIYDTSKLASGVPAHF 83
QY 62 SGSGSGTFTLEISRKAEDGVVYCCQLVEYPLTFGAGTKLELRADAAPTVSIF 117
DB 84 RSGSGTSYSLTISGMEADAATYYCQWSSNPFTEGSGTKLEINRADTAPTVSIF 139

RESULT 13

US-10-704-071-5
Sequence 5, Application US/10704071
Publication No. US20040076627A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Attwal, Diljeet S.
Emtage, John S.

TITLE OF INVENTION: Humanised Antibodies

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,071
FILING DATE: 07-Nov-2003
CLASSIFICATION: (D)

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,658
FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-704-071-5

Query Match 73.4%; Score 445; DB 15; Length 235;
Best Local Similarity 75.0%; Pred. No. 2.1e-33;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRIYDTSKLASGVPAEL 61
DB 24 IVLTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRIYDTSKLASGVPAHF 83
QY 62 SGSGSGTFTLEISRKAEDGVVYCCQLVEYPLTFGAGTKLELRADAAPTVSIF 117
DB 84 RSGSGTSYSLTISGMEADAATYYCQWSSNPFTEGSGTKLEINRADTAPTVSIF 139

RESULT 14

US-09-144-886-82
Sequence 82, Application US/09144886
Patent No. US2002015114A1
GENERAL INFORMATION:

APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins

FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 82

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone

OTHER INFORMATION: IE8 region VL epitope 1

US-09-144-886-82

Query Match 72.6%; Score 440; DB 9; Length 107;
Best Local Similarity 80.4%; Pred. No. 2.6e-33;
Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRIYDTSKLASGVPAAR 60
DB 1 DIELTQSPAIMSASPGKVTMTCSASSVNMHWFOESGTFPKRIYDTSKLASGVPAAR 60
QY 61 LSGSGSGTFTLEISRKAEDGVVYCCQLVEYPLTFGAGTKLELR 107
DB 61 FSGSGSGTSYSLTISGMEADAATYYCQWSSNPFTEGAGTKLELR 107


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RESULT 15
US-09-144-886-83
; Sequence 83, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: IG7 region VL epitope 1
US-09-144-886-83

Query Match      72.6%; Score 440; DB 9; Length 107;
Best Local Similarity 80.4%; Pred. No. 2.6e-33;
Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY      1 DIELTQSPAIMSASPGKVTWTCSSSSVNYMHWFQOESGTFPKRIYDTSKLAGVDPAR 60
Db      1 DIELTQSPAIMSASPGKVTWTCSSSSVNYMHWFQOESGTFPKRIYDTSKLAGVDPAR 60
QY      61 LSGSGSGTFTLEISRKAEDVGVVYCOOLVEYPLTFGAGTKLELKR 107
Db      61 FSGSGSGTYSYSLTSSMEAEADAATYYCQOWSSNPLTFGAGTKLELKR 107

Search completed: October 13, 2004, 13:15:27
Job time : 86.7792 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 12:48:23 ; Search time 24.7042 Seconds
(without alignments)
471.266 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPSQSLSI.....MITAYAMDYGQTTVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	552.5	87.0	141	2 S52446	Ig heavy chain V r
2	536	84.4	112	2 S11100	Ig heavy chain V r
3	533.5	84.0	117	2 S38563	Ig heavy chain V r
4	530.5	83.5	120	2 P00807	Ig heavy chain V r
5	529	83.3	140	2 S55028	Ig heavy chain V r
6	527	83.0	113	2 S11101	Ig heavy chain V r
7	527	83.0	114	2 S11106	Ig heavy chain V r
8	527	83.0	116	2 S11102	Ig heavy chain V r
9	524.5	82.6	139	2 A32456	Ig heavy chain pre
10	521	82.0	112	2 S11108	Ig heavy chain V r
11	517	81.4	115	2 S11103	Ig heavy chain V r
12	515	81.1	114	2 S11039	Ig heavy chain V r
13	507.5	79.9	116	2 S42484	Ig heavy chain V r
14	500.5	78.8	122	2 A49049	Ig heavy chain V r
15	500	78.7	106	2 S26322	Ig heavy chain V r
16	499	78.6	118	2 P00266	Ig heavy chain V r
17	497.5	78.3	135	2 S31913	Ig heavy chain V r
18	492.5	77.6	122	2 S20809	Ig gamma-2A chain
19	492	77.5	106	2 S14489	Ig heavy chain V r
20	492	77.5	114	2 S11105	Ig heavy chain V r
21	491	77.3	112	2 S11098	Ig heavy chain V r
22	490	77.2	117	2 S10111	Ig heavy chain V r
23	489	77.0	140	2 S14238	Ig gamma-1 chain p
24	487	76.7	127	2 B31807	Ig heavy chain V r
25	487	76.7	144	1 G2MS14	Ig heavy chain V r
26	486.5	76.6	118	2 S32786	Ig heavy chain pre
27	483	76.1	121	2 D30560	Ig heavy chain (an
28	480	75.6	121	2 S33131	Ig heavy chain V r
29	480	75.6	231	2 PC4155	Ig gamma-2b chain

30	479	75.4	109	2 S11109	Ig heavy chain V r
31	479	75.4	114	2 S11104	Ig heavy chain V r
32	478.5	75.4	144	2 S11244	Ig gamma-2a chain
33	477	75.1	107	2 S14492	Ig heavy chain V r
34	476	75.0	107	2 S14493	Ig heavy chain V r
35	475	74.8	100	2 S14490	Ig heavy chain V r
36	473	74.5	115	2 S11107	Ig heavy chain V r
37	471	74.2	111	2 S26324	Ig heavy chain V r
38	471	74.2	114	2 S26321	Ig heavy chain V r
39	470	74.0	107	2 S14491	Ig heavy chain V r
40	467.5	73.6	110	2 PH1024	Ig heavy chain V r
41	467	73.5	95	2 S17605	Ig heavy chain V r
42	464	73.1	110	2 S26323	Ig heavy chain V r
43	463	72.9	109	2 PH1025	Ig heavy chain V r
44	461.5	72.7	115	2 S26470	Ig heavy chain V r
45	455	71.7	101	2 S03466	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S52446
Ig heavy chain V region precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
R:Berdoz, J.; Kraehenbuhl, J.P.
A:Description: Specific amplification by the polymerase chain reaction of rearranged ge submitted to the EMBL Data Library, November 1994
A:Reference number: S52445
A:Accession: S52446
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <BER>
A:Cross-references: EMBL:X82692; NID:G673441; PIDN:CAA58013.1; PID:G673442
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match		87.0%	Score 552.5;	DB 2;	Length 141;
Best Local Similarity		89.3%	Pred. No. 3.1e-45;		
Matches 109;		Conservative 2;	Mismatches 10;	Indels 1;	Gaps 1;
Qy	1	QVQLQESGPGLVAPSQSLSI	TCVTSGISLNRYGVHVRQPPGKGLVGIWTCGSTNYN	60	
Db	20	QVQLKESGPGLVAPSQSLSI	TCVTSGFSLTSYGVHVRQPPGKGLGVWAGGSTNYN	79	
Qy	61	SALMSRLISKDNKSQVFLKMSLQDDTAMYYCARD-RSTMITAYAMDYGQTTVT	119		
Db	80	SALMSRLISKDNKSQVFLKMSLQDDTAMYYCARSPSTMDTPYAMDYGQTSVT	139		
Qy	120	SS 121			
Db	140	SS 141			

RESULT 2
S11100
Ig heavy chain V region (clone NQ2-20.5.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.P.; Milstein, C.
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11100
A:Molecule type: mRNA
A:Residues: 1-112 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 536; DB 2; Length 112;
Best Local Similarity 86.7%; Pred. No. 8.7e-44;
Matches 104; Conservative 1; Mismatches 7; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60
DB 1 QVQLKESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60

QY 61 SALMSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTSTVTS 120
DB 61 SALMSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTSTVTS 112

RESULT 3

IG heavy chain V region (ASW51) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38563
R:Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
A:Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A:Reference number: S38559
A:Accession: S38563
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <MON>
A:Cross-references: EMBL:X75099; NID:G414151; PIDN:CAA52990.1; PID:G414152
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 533.5; DB 2; Length 117;
Best Local Similarity 85.8%; Pred. No. 1.1e-43;
Matches 103; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60
DB 1 QVQLKESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60

QY 61 SALMSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTSTVTS 120
DB 61 SALKSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDG---YYDIAMDYWGQGTSTVTS 117

RESULT 4

PL0087

IG heavy chain V region (E3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0087
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J:Exp. Med. 169, 519-533, 1989
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A:Reference number: PL0080; NID:89094248; PMID:2492056
A:Accession: PL0087
A:Molecule type: mRNA
A:Residues: 1-120 <MEE>
A:Cross-references: GB:X58593; GB:Y00794; NID:G51571; PIDN:CAA41468.1; PID:G938252
A:Experimental source: strain BAB/c
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 530.5; DB 2; Length 120;
Best Local Similarity 86.0%; Pred. No. 3.1e-43;
Matches 104; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60

DB 1 QVQLKRSRGPGLVAPSSQSLISITCTVSGFSLTSSGVHVRPPGKGLEWLVITAGGSTNYN 60

QY 61 SALMSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTSTVTS 120
DB 61 SALMSRLTISKDNKSQVFLKMTSLQDITAMYYCARD-SHGQAYGVMDYWGQGTSTVTS 119

QY 121 S 121
DB 120 S 120

RESULT 5

S55028

IG heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C:Accession: S55028
R:Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff,
J. Mol. Biol. 248, 344-360, 1995
A:Title: Structure and specificity of the anti-digoxin antibody 40-50.
A:Reference number: S55027; MUID:95257394; PMID:7739045
A:Accession: S55028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <JEF>
A:Cross-references: EMBL:I31403; NID:G476717; PIDN:AAA38191.1; PID:G476718
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 529; DB 2; Length 140;
Best Local Similarity 82.6%; Pred. No. 5.1e-43;
Matches 100; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60
DB 20 QVHLKESGPGLVAPSSQSLISITCTVSGFSLTTVGVHVRPPGKGLEWLVITAGGSTNYN 79

QY 61 SALMSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTSTVTS 120
DB 80 SALMSRLSINKDNSKSOVFLKMNLSLQADITAMYYCARFRFASDYDYAVDYWGQGTSTVTS 139

QY 121 S 121
DB 140 S 140

RESULT 6

S11101

IG heavy chain V region (clone NQ2-48.2.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S11101
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolin
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 527; DB 2; Length 113;
Best Local Similarity 84.3%; Pred. No. 6.2e-43;
Matches 102; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRPPGKGLEWLVITGGSTNYN 60
DB 1 QVQLKESGPGLVAPSSQSLISITCTVSGKSLTSYGVHVRPPGKGLEWLVITAGGSTNYN 60

QY 61 SALMSRLSISKDNSKSOVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTSTVTS 120

Db 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDRGV-----YWGQGLTVTVS 112
121 S 121
113 A 113

RESULT 7
S11106
Ig heavy chain V region (clone N05-96.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11106
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11106
A:Molecule type: mRNA
A:Residues: 1-114 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 527; DB 2; Length 114;
Best Local Similarity 84.3%; Pred. No. 6.3e-43;
Matches 102; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

Qy 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLWGLVITWGSGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGISLTSGVHVRQPPGKGLWGLVITWGSGSTNYN 60
Qy 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDSTMITAYAMDYWGQGLTVTVS 120
Db 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARD-----GPAWGGTSTVTS 112
Qy 121 S 121
Db 113 S 113

RESULT 8
S11102
Ig heavy chain V region (clone N05-4.3.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11102
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11102
A:Molecule type: mRNA
A:Residues: 1-116 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 527; DB 2; Length 116;
Best Local Similarity 84.3%; Pred. No. 6.4e-43;
Matches 102; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

Qy 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLWGLVITWGSGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGISLTSGVHVRQPPGKGLWGLVITWGSGSTNYN 60
Qy 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDSTMITAYAMDYWGQGLTVTVS 120
Db 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDGX-----YWGQGLTVTVS 112
Qy 121 S 121
Db 113 A 113

RESULT 9
A32456
Ig heavy chain precursor V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C:Accession: A32456
R:Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A:Title: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin
A:Reference number: A32456; MUID:89174706; PMID:2494173
A:Accession: A32456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <DOM>
A:Cross-references: GB:J04609; NID:G556316; PIDN:AAA50298.1; PID:G556317
A:Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 524.5; DB 2; Length 139;
Best Local Similarity 85.0%; Pred. No. 1.3e-42;
Matches 102; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 2 VQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLWGLVITWGSGSTNYN 61
Db 21 VHLKESGPGLVAPSQSLITCTVSGISLTSGVHVRQPPGKGLWGLVITWGSGSTNYN 80
Qy 62 ALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDSTMITAYAMDYWGQGLTVTVS 121
Db 81 ALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCAK-RLERIFYAMDYWGQGLTVTVS 139

RESULT 10
S11108
Ig heavy chain V region (clone N05-78.2.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11108
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11108
A:Molecule type: mRNA
A:Residues: 1-112 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 521; DB 2; Length 112;
Best Local Similarity 84.2%; Pred. No. 2.3e-42;
Matches 101; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

Qy 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLWGLVITWGSGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGISLTSGVHVRQPPGKGLWGLVITWGSGSTNYN 60
Qy 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDSTMITAYAMDYWGQGLTVTVS 120
Db 61 SALMSRLSISKDNSKSVFLKXNSLQTDITAMYYCARDRE-----DIWGXGTSVTVS 112

RESULT 11
S11103
Ig heavy chain V region (clone N05-61.1.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11103
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353

A:Accession: S11103
A:Molecule type: mRNA
A:Residues: 1-115 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 517; DB 2; Length 115;
Best Local Similarity 83.5%; Pred. No. 5.6e-42; Indels 8; Gaps 1;
Matches 101; Conservative 2; Mismatches 10;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60
DB 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60

QY 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 120
DB 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 112

QY 121 S 121
DB 113 A 113

RESULT 12
S11099
Ig heavy chain V region (clone N02-17.4.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C:Accession: S11099
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11099
A:Molecule type: mRNA
A:Residues: 1-114 <NAT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 515; DB 2; Length 114;
Best Local Similarity 82.6%; Pred. No. 8.6e-42; Indels 8; Gaps 1;
Matches 100; Conservative 2; Mismatches 11;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60
DB 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60

QY 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 120
DB 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 112

QY 121 S 121
DB 113 A 113

RESULT 13
S42484
Ig heavy chain V region (4B1 VH) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S42484
R:Gilbert, D.; Brard, F.; Margairite, C.; Delpach, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A:Description: An idiotypic D23-bearing polypeptide, murine anti-DNA monoclonal antibody
A:Reference number: S42484
A:Accession: S42484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <GIL>
A:Cross-references: EMBL:Z30962; NID:g461325; PIDN:CAAB93216.1; PTD:g461326
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 507.5; DB 2; Length 116;
Best Local Similarity 80.3%; Pred. No. 4.5e-41; Indels 7; Gaps 2;
Matches 98; Conservative 6; Mismatches 11;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60
DB 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60

QY 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 119
DB 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 114

QY 120 SS 121

DB 115 SS 116

RESULT 14

A49049

Ig heavy chain V region (anti-idiotypic) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C:Accession: A49049

R:Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.

Eur. J. Immunol. 22, 2893-2899, 1992

A:Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen

A:Reference number: A49049; MUID:93049629; PMID:1425914

A:Accession: A49049

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-122 <ARM>

A:Experimental source: BALB/c

A:Note: sequence extracted from NCBI backbone (NCBI:118295, NCBIP:118296)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 500.5; DB 2; Length 122;

Best Local Similarity 81.8%; Pred. No. 2.2e-40; Indels 3; Gaps 2;

Matches 99; Conservative 6; Mismatches 13;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60

DB 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGGSTNN 60

QY 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 120

DB 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDSTMITAYAMDYWGQGTITV 117

QY 121 S 121

DB 118 S 118

RESULT 15

S26322

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C:Accession: S26322

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26322

A:Molecule type: mRNA

A:Residues: 1-106 <STA>

A:Cross-references: EMBL:X59182

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:9-91/Domain: immunoglobulin homology <IMM>

```

Query Match      78.7%; Score 500; DB 2; Length 106;
Best Local Similarity 85.1%; Pred. No. 2.1e-40;
Matches 97; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

QY 7 SGPGLVAPSQSLITCTVSGISLNRYGVHWVRQPPGKGLEWLGVIWGTGGSTNYSALMSR 66
Db 1 SGPGLVAPSQSLITCTVSGISLNRYGVHWVRQPPGKGLEWLGVIWGTGGSTNYSALMSR 60

QY 67 LSISKDNKSQVFLKXNSLQTDDTAMYCCARDRSTMITAYAMDYWGCGTTVTS 120
Db 61 LSISKDNKSQVFLKXNSLQTDDTAMYCCARE-----ALRLMGQGLTVTS 106

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Search completed: October 13, 2004, 13:00:06
Job time : 24.7042 secs

inis Page Blank (uspto)

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:47:33 ; Search time 121 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-10-049-868A-4

Perfect score: 635

Sequence: 1 QVQLQESGFLVAPQSLSI.....MITAVAMDYQGQITVTYSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.5	79.8	482	2	Q91X92 mus musculus
2	490.5	77.2	121	2	Q99NG4
3	487	76.7	144	1	HV43 MOUSE
4	442	69.6	115	1	HV44 MOUSE
5	436	68.7	116	1	HV45 MOUSE
6	401.5	63.2	135	1	HV02_XENLA
7	389.5	61.3	465	2	Q6GMX6
8	382	60.2	129	2	BAD00255
9	376	59.2	119	2	Q9UL73
10	373	58.7	121	1	HV33 HUMAN
11	371.5	58.5	620	2	Q96EY0
12	366	57.6	476	2	Q6GMX1
13	364.5	57.4	477	2	Q6GMX7
14	364.5	57.4	576	2	Q6P4I8
15	364.5	57.4	576	2	AAH63384
16	364	57.3	137	1	HV46 MOUSE
17	361.5	56.9	124	2	BAD00233
18	358.5	56.9	478	2	Q7Z379
19	356.5	56.1	573	2	Q8WU38
20	355	55.9	483	2	BACH85202
21	354	55.7	595	2	Q8WUX4
22	354	55.7	597	2	Q6GMX5
23	354	55.7	597	2	Q9BU10
24	354	55.7	625	2	Q96AA6
25	353.5	55.7	112	2	Q9HCC1
26	353	55.6	499	2	Q8NSK4
27	352	55.4	472	2	Q6N089
28	352	55.4	472	2	CAE45781
29	352	55.4	501	2	BAC85359
30	351	55.3	136	1	HV01_XENLA
31	350	55.1	120	2	BAD00465

32	350	55.1	128	2	BAD00406
33	348.5	54.9	122	1	HV3G_HUMAN
34	348	54.8	597	2	Q9BQB8
35	347	54.6	479	2	BAC85434
36	346	54.5	470	2	BAC85387
37	345.5	54.4	118	2	Q811U5
38	344.5	54.3	613	2	Q8WUK1
39	343	54.0	139	2	Q86SX2
40	342.5	53.9	120	2	AAJ35864
41	341.5	53.8	136	2	Q6LBU5
42	341.5	53.8	136	2	CAA34714
43	341	53.7	472	2	BAC85393
44	340	53.5	254	2	BAC86524
45	339.5	53.5	494	2	BAC85198

ALIGNMENTS

RESULT 1

Q91X92
ID Q91X92 PRELIMINARY; PRT; 482 AA.
AC Q91X92;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Heide F.,
Hopkins R.F., Jordan H., Moore K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RX Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL: BC011181; AAI11181.1; -
DR PIR; F33932; F33932.
DR HSP; P01820; IATN.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; P07654; C1-set; 2.
DR Pfam; P00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; P85083; IG_LIKE; 4.
DR PROSITE; P800290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 482 AA; 51864 MW; 312E01F9C1BC7F3C CRC64;

Bad00406 camelus d
P01768 homo sapien
Q9bqb8 homo sapien
Bac85434 homo sapi
Bac85387 homo sapi
Q811u5 mus musculu
Q8wuk1 homo sapien
Q86sx2 homo sapien
Aal35864 lama glam
Q6lbu5 mus musculu
Caa34714 mus muscu
Bac85393 homo sapi
Bac86524 homo sapi
Bac85198 homo sapi

```
Query Match 79.8%; Score 506.5; DB 2; Length 482;
Best Local Similarity 81.3%; Pred. No. 2.2e-44; Indels 7; Gaps 2;
Matches 100; Conservative 6; Mismatches 10; Indels 7; Gaps 2;

QY 1 QVQLQESGPGELVAPSSQSLISITCTVSGISLNRYGVHVRQPPGKGLVGLVITWGSGTNYN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLKESGPDIVAPSSQSLISITCTVSGFPALTSAISWVRQPPGKGLVGLVITWGVTNYN 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SALMSRLSISKDNKSQVFLKMNLSLQTDATMYCARDSTMITAY---AMDYWGQGTITVT 118
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SALKSRLSISKDNKSQVFLKMNLSLQTDATMYCARDSTMITAY---YEGAMDYWGQGTITVT 134
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 VSS 121
   |||||
Db 135 VSS 137
   |||||

RESULT 2
Q99NG4 PRELIMINARY; PRT; 121 AA.
AC Q99NG4;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OG Plasmid PHEN1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Arseniev L.,
RA Bartsch W., Kola A., Kloss A., Koehl J.;
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958 (1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR PIR; F33932; F33932.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 121 121
FT SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;

Query Match 77.2%; Score 490.5; DB 2; Length 121;
Best Local Similarity 79.3%; Pred. No. 2e-43; Indels 1; Gaps 1;
Matches 96; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQESGPGELVAPSSQSLISITCTVSGISLNRYGVHVRQPPGKGLVGLVITWGSGTNYN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLKESGPDIVAPSSQSLISITCTVSGFPALTSHGVSWRQPPGKGLVGLVITWGDTKYH 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SALMSRLSISKDNKSQVFLKMNLSLQTDATMYCARDSTMITAYAMDYWGQGTITVTS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SALISRLSISKDNKSQVFLKMNLSLQTDATMYCARDSTMITAYCAR-HYKYANYAMDYWGQGTITVTS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 S 121
   |
Db 120 S 120
   |

RESULT 3
HV43 MOUSE
ID HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
```

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DB Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683 (1980).
CC -!- MISCELLANEOUS: The sequence shown is translated from a
CC differentiated gene isolated from a myeloma that secretes IgD2b.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00491; AAA38121.1; -.
DR PIR; A02094; G2MS14.
DR HSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 Ig heavy chain V region MOPC 141.
FT DOMAIN 20 130 Ig-like.
FT NON_TER 144 144
FT SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 76.7%; Score 487; DB 1; Length 144;
Best Local Similarity 75.8%; Pred. No. 5.8e-43; Indels 10; Gaps 2;
Matches 97; Conservative 7; Mismatches 14; Indels 10; Gaps 2;

QY 1 QVQLQESGPGELVAPSSQSLISITCTVSGISLNRYGVHVRQPPGKGLVGLVITWGSGTNYN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLKESGPGELVAPSSQSLISITCTVSGFSLTGYVNVVRQPPGKGLVGLVITWGSGTNYN 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SALMSRLSISKDNKSQVFLKMNLSLQTDATMYCARDSTMITAY-----AMDYWGQ 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 STLSRLTITKDNKSQVFLKMNLSLQTDATARYCA---SVSIYYGRSDKYFTLDYWGQ 136
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 GTTVTVSS 121
   ||:|||||
Db 137 GTSVTVSS 144
   ||:|||||

RESULT 4
HV44_MOUSE
ID HV44_MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
```

RA Sakano H., Maki R., Kurosawa Y., Roeder W., Toneyawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes.";
 RL Nature 286:676-683(1980).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; V00767; CAA24148.1; -
 DR PIR; A02095; HWS14.
 DR PDB; 1A7N; X-ray; H=20-115.
 DR PDB; 1A7O; X-ray; H=20-115.
 DR PDB; 1A7P; X-ray; H=20-115.
 DR PDB; 1A7R; X-ray; H=20-115.
 DR PDB; 1G7H; X-ray; B=20-115.
 DR PDB; 1G7I; X-ray; B=20-115.
 DR PDB; 1G7J; X-ray; B=20-115.
 DR PDB; 1G7M; X-ray; B=20-115.
 DR PDB; 43C9; X-ray; B/D/F/H=19-115.
 DR PDB; 43CA; X-ray; B/D/F/H=20-115.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW 3D-structure; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 115 Ig heavy chain V region PJ14.
 FT DOMAIN 20 >115 Ig-like.
 FT STRAND 22 26
 FT STRAND 30 30
 FT STRAND 37 44
 FT TURN 48 49
 FT TURN 52 58
 FT TURN 60 61
 FT STRAND 65 70
 FT TURN 72 73
 FT STRAND 76 78
 FT TURN 80 82
 FT STRAND 83 85
 FT STRAND 86 91
 FT HELIX 92 94
 FT TURN 95 95
 FT STRAND 96 101
 FT HELIX 106 108
 FT STRAND 110 115
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
 Query Match 69.6%; Score 442; DB 1; Length 115;
 Best Local Similarity 88.5%; Pred. No. 2.3e-38;
 Matches 85; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHVVRRQPGKGLWLVITGGSTNNY 60
 Db 20 QVQLKQSGPGLVAPSQSLSTCTVSGISLNRYGVHVVRRQPGKGLWLVITGGSTNNY 79
 QY 61 SALMSRLSISKDNSKSOVFLKMSLQTDITAMYYCAR 96
 Db 80 SALMSRLSISKDNSKSOVFLKMSLQTDITAMYYCAR 115
 RESULT 5
 HV45 MOUSE
 ID HV45_MOUSE STANDARD; PRT; 116 AA.
 AC P01821;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MC101 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82075900; PubMed=6273429;
 RA Katsuka T., Nikaide T., Miyata T., Moriaki K., Honjo T.;
 RT "The nucleotide sequences of rearranged and germ-line immunoglobulin VH
 genes of a mouse myeloma MC101 and evolution of VH genes in mouse.";
 RL J. Biol. Chem. 257:277-285(1982).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 CC EMBL; J00502; AAA38515.1; -
 DR PIR; A02096; GLMS10.
 DR HSSP; P01820; IG7J.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 116 Ig heavy chain V region MC101.
 FT DOMAIN 20 >116 Ig-like.
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;
 Query Match 68.7%; Score 436; DB 1; Length 116;
 Best Local Similarity 83.5%; Pred. No. 1e-37;
 Matches 81; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHVVRRQPGKGLWLVITGGSTNNY 60
 Db 20 QVQLKQSGPGLVAPSQSLSTCTVSGISLNRYGVHVVRRQPGKGLWLVITGGSTNNY 79
 QY 61 SALMSRLSISKDNSKSOVFLKMSLQTDITAMYYCAR 97
 Db 80 AAPISRLSISKDNSKSOVFLKMSLQTDITAMYYCAR 116
 RESULT 6
 HV02 XENLA
 ID HV02_XENLA STANDARD; PRT; 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88176921; PubMed=2451244;
 RA Schwager J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis IGM deduced
 from cDNA sequence: implications for evolution of immunoglobulin
 domains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).

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CC  -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL: J03632; AAA49791.1; -.
CC PIR: B31933; B31933.
CC HSSP: P01820; IATN.
CC DR InterPro: IPR007110; Ig-like.
CC DR InterPro: IPR003596; Ig_v.
CC DR Pfam: PF00047; Ig; 1.
CC DR SMART: SM00406; IGV; 1.
CC DR PROSITE: PS50835; IG LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC KW NON_TER 1
CC FT SIGNAL <1 18
CC FT CHAIN 19 135
CC FT DOMAIN 20 128
CC FT NON_TER 135 135
CC SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 63.2%; Score 401.5; DB 1; Length 135;
Best Local Similarity 61.9%; Pred. No. 4.9e-34;
Matches 73; Conservative 19; Mismatches 23; Indels 3; Gaps 1;

QY 4 LOESGPGVLVAPQSLSITCTVSGISINRYGVHWRQPPGKGLWLGVIWGTGGSTNVNSAL 63
DB 21 LOESGPGVTKPSESRLTCTVSGFELSSVHMHWRQPPGKGLWLGVIWGTGGSTNVNSAL 80
QY 64 MSRLSKDNKSQVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTIVTVSS 121
DB 81 KNRVITKDKGKKQVYLQWNGVEVKDTAMYYCAREYA---SGYNFDYWGQGTIVTVSS 135

RESULT 7
O6GMX6 PRELIMINARY; PRT; 465 AA.
AC O6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073766; AAH73766.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 3.
DR SMART: SM00403; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 61.3%; Score 389.5; DB 2; Length 465;
Best Local Similarity 62.8%; Pred. No. 3.8e-32;
Matches 76; Conservative 17; Mismatches 23; Indels 5; Gaps 1;

QY 1 QVQLQESGPGVLVAPQSLSITCTVSGISINRYGVHWRQPPGKGLWLGVIWGTGGSTNVN 60
DB 20 QVQLQESGPGVLVAPQSLSITCTVSGISINRYGVHWRQPPGKGLWLGVIWGTGGSTNVN 79
QY 61 SALMSRLSKDNKSQVFLKMNLSLQTDITAMYYCARDSTMITAYAMDYWGQGTIVTVSS 120
DB 80 PSLKSRVIMSVDTSKNQSLSLSSVTAADTAVVYCARGRTY-----FDYWGQGTIVTVSS 134
QY 121 S 121
DB 135 S 135

RESULT 8
BAD00255 PRELIMINARY; PRT; 129 AA.
AC BAD00255;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VH D region (Fragment).
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB091893; BAD00255.1; -.
DR NON_TER 1
DR NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D9642F5A5B3BEE CRC64;

Query Match 60.2%; Score 382; DB 2; Length 129;
Best Local Similarity 58.1%; Pred. No. 5.2e-32;
Matches 75; Conservative 20; Mismatches 26; Indels 8; Gaps 2;

QY 1 QVQLQESGPGVLVAPQSLSITCTVSG--ISLNRYGVHWRQPPGKGLWLGVIWGTGGSTN 58
DB 1 QVQLQESGPGVLVAPQSLSITCTVSG--ISLNRYGVHWRQPPGKGLWLGVIWGTGGSTN 60

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QY 59 YNSALMSRLSISKDQSKVFLKMSLQTDITAMYYCARDR-----STMITAYAMDYWG 112
Db 61 YGSLKSRYSFSDTSKQFSLQSSVTPEDTAVYYCARDSPRLRVSRSRGVSYMDYWG 120
QY 113 QGTVTVSS 121
Db 121 KGLTVTISS 129

RESULT 9
Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSP; P01820; IG73.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB8656420EA0BE CRC64;

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Query Match 59.2%; Score 376; DB 2; Length 119;
Best Local Similarity 62.0%; Pred. No. 2e-31;
Matches 75; Conservative 15; Mismatches 29; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPKGLWLGVIWTGGSNTYN 60
Db 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPKGLWLGVIWTGGSNTYN 60
QY 61 SALMSRLSISKDQSKVFLKMSLQTDITAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db 61 PSLKSRVTSVDRSKNQFSLKLSLTAAADTAVYCA--RLSNWGPYPFDYWGQGLTVTVS 118
QY 121 S 121
Db 119 S 119

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RESULT 10
HV3J_HUMAN STANDARD; PRT; 121 AA.
ID HV3J_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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```

RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG Hil.";
RL Biochemistry 18:553-560(1979).
CC !- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC !- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02054; GIHULH.
DR HSP; P01772; 2FB4.
DR GO; GO:005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 121
FT NON_TER 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

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Query Match 58.7%; Score 373; DB 1; Length 121;
Best Local Similarity 54.9%; Pred. No. 4.2e-31;
Matches 67; Conservative 26; Mismatches 27; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPKGLWLGVIWTGGS-TNY 59
Db 1 QVQLQAGGVVQPGSRSLRSLSCISAGFTFSNGHVRQAPKGLWVAVIYNGSRYY 60
QY 60 NSALMSRLSISKDQSKVFLKMSLQTDITAMYYCARDRSTMITAYAMDYWGQTTVTV 119
Db 61 GDSVKGRTISRDNSKRTLYMZMNSLRTEITAVYYCARD-PDILTAFSDYWGQGLTVTV 119
QY 120 SS 121
Db 120 SS 121

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RESULT 11
Q96EY0 PRELIMINARY; PRT; 620 AA.
ID Q96EY0
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AAH11857.2; --
 DR PIR; S15590; S15590.
 DR HSSP; P01820; IG73.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 4.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 4.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00407; IGcl; 3.
 DR PROSITE; PS0835; IG LIKE; 5.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN 3.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN 3.
 SQ SEQUENCE 620 AA; 68125 MW; 990A14AA6E8FF27B CRC64;

Query Match 58.5%; Score 371.5; DB 2; Length 620;
 Best Local Similarity 60.3%; Pred. No. 4.1e-30;
 Matches 73; Conservative 19; Mismatches 28; Indels 1; Gaps 1;
 QY 1 QVQLQESGPGLVAPQSQSLITCTVSGISLNRYGVHVRQPPGKGLWLVGTGGSTNN 60
 DB 27 QVQLQESGPGLVAPQSQSLITCTVSGISLNRYGVHVRQPPGKGLWLVGTGGSTNN 86
 QY 61 SALMERLSISKDNKSKQVFLKMSLQTDITAMYYCARDSTMTITAYMDYWGQGITVTVS 120
 DB 87 PSLKSRVMSVDTSKNQFSLKMSVTAADTAVYFCARAGVWGSFRAIDGF--NIWG 145
 QY 121 S 121
 DB 146 S 146

RESULT 12
 Q6GMX1 PRELIMINARY; PRT; 476 AA.
 ID Q6GMX1
 AC Q6GMX1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073773; AAH73773.1; --
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 57.6%; Score 366; DB 2; Length 476;
 Best Local Similarity 60.5%; Pred. No. 1.1e-29;
 Matches 78; Conservative 14; Mismatches 27; Indels 10; Gaps 3;
 QY 1 QVQLQESGPGLVAPQSQSLITCTVSG--ISLNRYGVHVRQPPGKGLWLVGTGGSTN 58
 DB 20 QVQLQESGPGLVAPQSQSLITCTVSGGSISSGDIYWSMIRQPPGKGLWLVGTGGSTV 79
 QY 59 YNSALMSRLSISKDNKSKQVFLKMSLQTDITAMYYCARD-----RSTMTAYAMDYWG 112
 DB 80 YNPSLKSRVTISLDTSKNQFSLKMSVTAADTAVYFCARAGVWGSFRAIDGF--NIWG 137
 QY 113 QGTTVTSS 121
 DB 138 QGTMVTSS 146

RESULT 13
 Q6GMX7 PRELIMINARY; PRT; 477 AA.
 ID Q6GMX7
 AC Q6GMX7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Search completed: October 13, 2004, 12:59:13
Job time : 123 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:44:23 ; Search time 112.933 Seconds
(without alignments)
384.353 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPSSLSL.....MITAYADYWGQGTIVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 359729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	87.7	113	2	AAR21268 Murine VH
2	555	87.4	115	8	ADF77174
3	553	87.1	125	6	ABR44627 Murine va
4	547	86.1	667	6	ABP97414 Anti-huma
5	546	86.0	253	5	AAU72867 PS-9 sing
6	541.5	85.3	120	4	AAG63986 Amino aci
7	538	84.7	222	2	AAR32843 VH NQ2/12
8	538	84.7	235	2	AAR32840 VH NQ2/12
9	537	84.6	142	4	AAG66520 Mouse ant
10	535	84.3	119	2	AAV49218 Heavy cha
11	535	84.3	119	6	ADA14778 Peptide f
12	535	84.1	119	7	ADC35320 Anti-IDIO
13	534	84.1	123	2	AAU07438 Anti-DNA
14	534	84.1	269	2	AAR32569 Fusion pr
15	532	83.8	476	4	AAAB49243 Chimeric
16	531.5	83.7	140	2	AAW22538 Murine an
17	531.5	83.7	140	5	AAE20201 Murine 44
18	531.5	83.7	140	8	ADJ31875 Murine 44
19	526	82.8	119	5	AAU72838 Anti-NGK2
20	525.5	82.8	242	2	AAR06483 18-2-3-T
21	525.5	82.8	242	2	AAR43680 Single ch
22	525.5	82.8	242	2	AAR99650 Single ch
23	525.5	82.8	242	2	AAW02192 18-2-3/TR
24	523	82.4	119	2	AAW42451 Mouse ant
25	522.5	82.3	247	8	ADG28588 Paramyxov

26	522.5	82.3	287	6	ABR42057
27	522.5	82.3	543	7	ADD12876
28	521.5	82.1	112	2	AAW31648
29	521.5	82.1	239	2	AAW02191
30	521.5	82.1	241	2	AAR06482
31	521	82.0	121	7	ADD25691
32	521	82.0	271	7	ADD25693
33	521	82.0	556	7	ADD25707
34	520.5	82.0	239	2	AAR43679
35	520.5	82.0	239	2	AAR99649
36	519	81.7	119	6	ABU19263
37	519	81.7	279	6	ABJ19275
38	518.5	81.7	116	2	AAR40951
39	518	81.6	119	2	AAR98478
40	517.5	81.5	116	4	AAU07513
41	517.5	81.5	239	2	AAW09813
42	517.5	81.5	239	2	AAW35561
43	517.5	81.5	241	2	AAR21261
44	517.5	81.5	267	2	AAR04841
45	517.5	81.5	272	2	AAR21260

ALIGNMENTS

RESULT 1
AAR21268

ID AAR21268 standard; protein; 113 AA.

XX AAR21268;

XX AC

XX 21-MAY-1992 (first entry)

XX Murine VH group 2 chain E specific for phOx.

DE Fd; bacteriophage; Gene III; filamentous; phagemid; capsid; coat; pilus;
KW g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX Synthetic.

OS

XX Key

XX Binding-site

XX Location/Qualifiers

XX 31..35

XX /label= CDR1

XX Binding-site

XX 50..65

XX /label= CDR2

XX Binding-site

XX 98..102

XX /label= CDR3

XX /note= "D/N-X-X-X motif "

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990;

XX 90GB-00015198.

XX 10-JUL-1990;

XX 90GB-00015198.

XX 19-OCT-1990;

XX 90GB-00022845.

XX 12-NOV-1990;

XX 90GB-00024503.

XX 06-MAR-1991;

XX 91GB-00004744.

XX 15-MAY-1991;

XX 91GB-00010549.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX (MEDI-) MED RES COUNCIL.

XX PA

XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;

XX Jackson RH, Holliger KP, Marks JD;

XX WPI; 1992-056862/07.

XX Producing members of specific binding pairs - by expression in

XX recombinant host cells with a secreting replicable genetic display

XX package.

XX PT

XX Example 21; Fig 24; 209pp; English.
 XX The VH sequence is one of eight (AAR21264-71) found to be expressed from
 CC a single chain Fv library from an immunised mouse. The library produces a
 CC diverse repertoire of antibody fragments specific for 2-phenyl-5-
 CC oxazolone (phOx). It was prep'd. using cDNA generated from mRNA from mice
 CC immunised with phOx coupled to chicked serum albumin. The VH and VL kappa
 CC sequences were separately amplified by PCR (see AAQ23474-84) and ligated
 CC into fCAr2 (see AAQ23463) for expression on the phage surface as fusions
 CC with gene III. The resulting library of clones was diverse. Twenty three
 CC hapten binding clones were sequenced revealing the eight different VH
 CC genes (A-H) in a variety of pairings with seven different Vκ genes (a-g)
 CC (see AAR21264-92). Nearly all the VH genes belonged to gp 1, with only
 CC one, "E", being of gp 2 (VHox1). Of the twenty three clones sequenced,
 CC only one was of type "E". Most of the clones were Vκ-d combinations. The
 CC Kd of VH-B/Vκ-d for phOx-GABA was 10 nM. Only two other combinations (of
 CC eleven tested) were found to have higher values. This suggests that phage
 CC bearing scFv fragments having weak affinities can be selected with
 CC the phage. See also AAR21260-307, 309-311; AAR22450, 565-581
 XX Sequence 113 AA;

Query Match 87.7%; Score 557; DB 2; Length 113;
 Best Local Similarity 89.3%; Pred. No. 4.8e-44;
 Matches 108; Conservative 0; Mismatches 5; Indels 8; Gaps 1;
 QY 1 QVQLQESGPGGVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWGGSTNNY 60
 DB 1 QVQLQESGPGGVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWGGSTNNY 60
 QY 61 SALMSRLSISKNSKQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTS 120
 DB 61 SALMSRLSISKNSKQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTS 112
 QY 121 S 121
 DB 113 S 113

RESULT 2
 ADF77174
 ID ADF77174 standard; protein; 115 AA.
 XX ADF77174;
 AC ADF77174;
 XX 26-FEB-2004 (first entry)
 DT Anti-VAP-1 monoclonal antibody Mo1G6 H chain.
 XX complementarity determining region; CDR; mouse;
 KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
 KW chimeric; inflammatory disorder; rheumatoid arthritis;
 KW inflammatory bowel disease; autoimmune disease; psoriasis;
 KW immunoscintigraphic imaging.
 XX Mus sp.
 OS WO2003093319-A1.
 XX 13-NOV-2003.
 PD 28-APR-2003; 2003WO-FI000330.
 XX 29-APR-2002; 2002FI-00000807.
 XX (BIOT-) BIOTIE THERAPIES CORP.
 PA Jalkanen S, Salmi M, Laukkanen M, Clark MR;
 PI WPI; 2004-022642/02.
 XX Ablating/killing aberrant prostate specific membrane antigen-expressing

PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
 PT encoding nucleic acid molecules, useful for diagnosing and treating
 PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
 XX Disclosure; Fig 1; 56pp; English.
 PS This sequence represents a heavy chain variable region from a mouse anti-
 CC Vascular Adhesion Protein-1 (VAP-1) antibody. This sequence is included
 CC in the specification for comparison with the antibody of the invention.
 CC The murine antibody sequences of the invention may be used in the
 CC production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic
 CC acid molecules, polypeptides or antibodies are useful in treating VAP-1
 CC mediated inflammatory disorders, such as rheumatoid arthritis, The
 CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
 CC chimeric VAP-1 antibody is further used for in vitro and in vivo
 CC diagnostic applications, including in vivo immunoscintigraphic imaging of
 CC inflammation sites. The chimeric MAb's of the invention have improved
 CC kinetic properties compared to the corresponding murine antibodies.
 XX Sequence 115 AA;

Query Match 87.4%; Score 555; DB 8; Length 115;
 Best Local Similarity 87.6%; Pred. No. 7.5e-44;
 Matches 106; Conservative 4; Mismatches 5; Indels 6; Gaps 1;
 QY 1 QVQLQESGPGGVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWGGSTNNY 60
 DB 1 QVQLQESGPGGVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWGGSTNNY 60
 QY 61 SALMSRLSISKNSKQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTS 120
 DB 61 SALMSRLSISKNSKQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTS 114
 QY 121 S 121
 DB 115 S 115

RESULT 3
 ABR44627
 ID ABR44627 standard; protein; 125 AA.
 XX ABR44627;
 AC ABR44627;
 XX 25-JUL-2003 (first entry)
 DT Marine variable heavy chain amino acid sequence MuVHIB.
 XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 KW neoplastic disorder.
 XX Mus musculus.
 OS Synthetic.
 XX WO2003024388-A2.
 XX 27-MAR-2003.
 PD 30-MAY-2002; 2002WO-US017204.
 XX 20-SEP-2001; 2001US-0324100P.
 PR 08-MAR-2002; 2002US-0362612P.
 XX (CORR) CORNELL RES FOUND INC.
 PA Bander N;
 XX WPI; 2003-313319/30.
 XX Ablating/killing aberrant prostate specific membrane antigen-expressing

cells for treating skin disorders, by contacting the cell with an antibody that binds to the extracellular domain of prostate specific membrane antigen.

Disclosure; Fig 12B; 225pp; English.

The present invention describes a method (M1) for ablating or killing an aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g. an epidermal and a dermal cell). M1 comprises contacting the cell, or a vascular endothelial cell proximate to the cell, with an antibody (or its antigen-binding fragment), which binds specifically to the extracellular domain of PSMA in an amount sufficient to ablate or kill the cell. The antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic antiinflammatory and antiallergic activities, and can be used in vaccines. M1 is useful for treating a skin disorder in a subject, by administering to the subject, an amount of an antibody which binds specifically to the extracellular domain of PSMA (the subject is a mammal, preferably human and is having, or at risk of, a skin disorder). The skin disorder is a dermal or an epidermal disorder, and is selected from psoriasis (preferably chronic stationary psoriasis, and is selected vulgaris, eruptive (glutatie) psoriasis, psoriatic erythroderma, generalised pustular psoriasis (Von Zumbusch), annular pustular, psoriasis, and localised pustular psoriasis), psoriatic arthritis, exfoliative dermatitis, pityriasis rubra pilaris, pityriasis roseacea, parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus, ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis, preferably psoriasis. M1 is useful for treating a skin disorder such as an inflammatory or neoplastic disorder of the epidermis or dermis, preferably an epidermal precancerous or cancerous lesion. M1 is also useful to treat or prevent disorders involving aberrant activity of PSMA-expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837 and ABR44613 to ABR44733 represent sequences used in the exemplification of the present invention

Sequence 125 AA;

Query Match 87.1%; Score 553; DB 6; Length 125;
Best Local Similarity 87.2%; Pred. No. 1.3e-43;
Matches 109; Conservative 3; Mismatches 9; Indels 4; Gaps 2

QY 1 QVQLQESGGPGGVAPSQSLSTCTVSGISLNRYGH--WROPPOKGLEWLGIWTGGSTN 58
| | | : | | | | | | | | | | | | | | | | | |
Db 1 QVQKESGPGGLVAPSQSLSTCTVSGFSLTSGYHVSWVRPPKGLEWLGIWAGGSTN 60
| | | | | | | | | | | | | | | | | | | | | |
QY 59 YNSALMSRLGISKDNSKSQVFLKNWSLQTDDTAMYYCARDSEMTITA--YAMDYWGQGT 116
| | | | | | | | | | | | | | | | | | | | | |
Db 61 YNSALMSRLGISKDNSKSQVFLKNWSLQTDDTAMYYCARDGRYYYSGYYANDYWGQTS 120
| | | | | | | | | | | | | | | | | | | | | |
QY 117 VTVSS 121
| | | | | | | | | | | | | | | | | | | | | |
Db 121 VTVSS 125
| | | | | | | | | | | | | | | | | | | | | |

RESULT 4	
ABP97414	ABP97414
XX	ABP97414 standard; protein; 667 AA.
XX	AC
XX	ABP97414;
XX	DT
XX	30-MAY-2003 (first entry)
XX	Anti-human seminal plasma protein ScFv/hCPA fusion protein.
DE	
XX	
KW	Single chain antibody; ScFv; anti-human seminal plasma protein;
KW	monoclonal antibody E4B7; mouse; murine; human; carboxypeptidase A; hCPA;
KW	fusion protein; antibody-directed enzyme prodrgug therapy; ADEPT;
KW	methotrexate-alpha-peptide prodrgug; prostate cancer; cytostatic; gene;
KW	ds.
XX	
OS	Mus musculus.
OS	Homo sapiens.
OS	Synthetic.
OS	Chimeric.

XX			
PH	Key	Location/Qualifiers	
FT	Protein	1..245	
FT		/label= E4B7 derived_ScFv	
FT		/note= "Anti-human seminal plasma protein single chain	
FT		antibody derived from murine monoclonal antibody E4B7 VH	
FT		and VL regions; targets fusion protein to prostate cancer	
FT		cells"	
FT	Region	1..122	
FT		/note= "Corresponds to monoclonal antibody E4B7 VH (heavy	
FT		chain variable region"	
FT	Region	123..137	
FT		/label= ScFv_linker	
FT	Region	138..245	
FT		/note= "Corresponds to monoclonal antibody E4B7 VL (light	
FT		chain variable region"	
FT	Misc-difference	216	
FT		/note= "Encoded by GAC"	
FT	Region	245..251	
FT		/label= ScFv/hCPA_linker	
FT	Misc-difference	247	
FT		/note= "Encoded by AGC"	
FT	Protein	253..667	
FT		/label= hCPA	
FT		/note= "Human carboxypeptidase A; activates methotrexate-	
FT		alpha-peptide produg"	
FT			

PN WO2002100431-A1.
 XX
 XX
 PD 19-DEC-2002.
 XX
 XX
 PF 08-JUN-2001; 2001WO-CN000924.
 XX
 XX
 PR 08-JUN-2001; 2001WO-CN000924.
 XX
 XX
 PA (UJTA-) UNIV TANGDU HOSPITAL FORTH MILITARY MEDI.
 PA (HAOX/) HAO X.
 XX
 XX
 PI Hao X;
 XX
 XX
 DR WPI; 2003-156924/15.
 DR N-PSDB; ABZ75116.
 XX
 XX
 PT Pharmaceuticals kits for use in the treatment of prostate cancer, comprise
 PT anti-human seminal plasma protein single-chain antibody/human
 PT carboxypeptidase fusion protein and a prodrug of methotrexate-alpha-
 PT peptides.

Claim 3; Fig 4; 29pp; Chinese.

The invention relates to a pharmaceutical kit for antibody-directed enzyme prodrug therapy (ADEPT) to treat prostate cancer. The kit comprises several respective containers for holding anti-human seminal plasma protein single-chain antibody (ScFv)/human carboxypeptidase A (hCPCA) fusion protein (ABP97414), a prodrug of methotrexate-alpha-peptide and a pharmaceutically-acceptable auxiliary for medication. The invention also encompasses the anti-human seminal plasma protein ScFv/hCPCA fusion protein, and the nucleic acid encoding it (ABZ75116). This was constructed by linking DNA encoding the ScFv (itself generated by linking DNAs encoding the heavy and light chain variable regions (VH and VL) of the murine anti-human seminal plasma protein monoclonal antibody E4B7) to DNA encoding human carboxypeptidase A via a linker. The ScFv portion of the fusion protein enables it to be specifically targeted to prostate cancer cells, where the hCPCA portion can then activate the prodrug which in turn has cytostatic activity towards the cancer cells. The invention permits the fusion protein to be easily produced in large quantities for use in ADEPT for prostate cancer treatment. The present sequence represents the ScFv/hCPCA fusion protein of the invention

Sequence 667 AA;

Query Match	86.1%	Score 547;	DB 6;	Length 667;
Best Local Similarity	86.8%	Pred. No. 3e-42;		

Matches 105; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLQESGPGHIVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWTGSGTNYN 60
Db 2 QVQLQESGPGHIVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWTGSGTNYN 61

QY 61 SALMSRLSISKDNKSQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTVS 120
Db 62 SALMSRLSISKDNKSQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTVS 119

QY 121 S 121
Db 120 S 120

RESULT 5
AAU72867
ID AAU72867 standard; protein; 253 AA.
XX AC AAU72867;
XX DT 26-FEB-2002 (first entry)
XX DE P5-9 single chain Fv.
XX KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7B7;
KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; P4-2; P4-3; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
XX OS Homo sapiens.
XX PN WO200171005-A2.
XX PD 27-SEP-2001.
XX PF 26-MAR-2001; 2001WO-EP003414.
XX PR 24-MAR-2000; 2000EP-00106467.
XX PA (KUFE/) KUFER P.
XX PI Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
PI Mayer M, Hofmeister R;
XX WPI; 2002-055119/07.
DR N-PSDB; AAS97141.
XX Multifunctional polypeptides comprising binding sites that specifically
PT recognize extracellular groups of the NKG2D receptor complex and domains
PT which function as receptors or ligands, useful for treating cancers and
PT infectious diseases.

Example 7; Fig 16; 114pp; English.

The invention relates to a multifunctional polypeptide comprising a
domain with a binding site that specifically recognises an extracellular
group of the NKG2D receptor complex and a second domain which functions
as a receptor or ligand. The polypeptide and its associated
polynucleotide are used for the preparation of a pharmaceutical
composition for the treatment of cancer, infections and/or autoimmune
conditions. The cancer may be a tumour of the head and neck, stomach,
oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
The infectious diseases can be caused by viruses, bacteria, fungi,
protozoa or helminths. The autoimmune diseases include multiple
sclerosis, Grave's disease, ankylosing spondylitis, acute anterior

uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
receptor and the polypeptides of the invention

XX Sequence 253 AA;
Query Match 86.0%; Score 546; DB 5; Length 253;
Best Local Similarity 88.5%; Pred. No. 1.2e-42;
Matches 108; Conservative 2; Mismatches 8; Indels 4; Gaps 2;

QY 1 QVQLQESGPGHIVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWTGSGTNY 59
Db 1 EVQLLESGPGHIVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWTGSGTNY 60

QY 60 NSALMSRLSISKDNKSQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTV 119
Db 61 NSALMSRLSISKDNKSQVFLKNSLQTDITAMYYCARDSTMITAYAMDYWGQGTITVTV 117

QY 120 SS 121
Db 118 SS 119

RESULT 6
AAG63986
ID AAG63986 standard; protein; 120 AA.
XX AC AAG63986;
XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of heavy chain variable region of antibody 2C4.
XX KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX OS Mus sp.
XX PN WO200166126-A1.
XX PD 13-SEP-2001.
XX PF 05-MAR-2001; 2001WO-US007193.
XX PR 07-MAR-2000; 2000US-0187595P.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX WPI; 2001-570749/64.
DR N-PSDB; AAH78183.
XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal.
XX Claim 17; Fig 1; 35pp; English.
XX The present sequence represents the heavy chain variable region of murine
CC monoclonal antibody 2C4. This antibody binds to human sialoadhesin factor
CC -2 (SAF-2). The antibody is useful for treating or preventing allergic
CC rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma,
CC leukemia or systemic mastocytosis in a mammal. It is also useful for
CC detecting the presence of a cell, especially eosinophil in a sample, by
CC detecting binding of the antibody to SAF-2. The antibody can be coupled
CC to toxins, antiproliferative drugs or radionuclides to kill cells in
CC areas of excessive SAF-2 expression

```

XX SQ Sequence 120 AA;
    Query Match      85.3%; Score 541.5; DB 4; Length 120;
    Best Local Similarity 86.0%; Pred. No. 1.4e-42;
    Matches 104; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHWRQPPGKGLEWLGVIWGGSTNN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTIVGAHWVRQPPGKGLEWLGVIWAGGSTNN 60

QY 61 SALMSRLSISKDNKSKQVFLKMNLSIQDQDTAMYYCARDSTMITAYAMDYWGQGTIVTVS 120
Db 61 SALMSRLSISKDNKSKQVFLKMNLSIQDQDTALYYCARDGSPY-YYSMEYWGQGTIVTVS 119

QY 121 S 121
Db 120 S 120

RESULT 7
AAR32843
ID AAR32843 standard; protein; 222 AA.
XX
AC AAR32843;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1993 (first entry)
XX
DE VH NQ2/12.4-Vk NQ10/12.5 linked peptide sequences #2.
XX
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazalone; hybridoma;
KW NQ2/12.4; NQ10/12.5.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..113
FT Peptide /label= VH_NQ2/12.4
FT Peptide 114..115
FT Region /note= "Linker peptide"
FT Region 116..222
FT /label= Vkappa_NQ2/12.4
XX
PN WO9303151-A1.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-GB001483.
XX
PR 10-AUG-1991; 91GB-00017352.
PR 11-JUN-1992; 92GB-00012419.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Embleton MJ, Gorochov G, Jones PT, Winter GP;
XX
XX WPI; 1993-076508/09.
DR N-PSDB; AAQ37462.
XX
PT Treatment of cell populations, partic. hybridomas - to link together
PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
PS Disclosure; Fig 5; 72pp; English.
XX

The sequences given in AAR32840-43 show the mature heavy chain VH domains
and the Vk light chain genes of the antiphenyloxazalone hybridomas
NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
cell PCR. The cDNA encoding these peptides was synthesised using forward
primers annealing to the Ck gene and the JH segment, followed by assembly
with linker primers, VH back primers based on the VH3 leader sequence and

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CC a forward Ck primer nested in respect to the primer used for cDNA. The
CC assembled product within the cells is then amplified with nested primers
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC In-cell PCR may be used to determine gene linkage analysis, particularly
CC for the cloning of gene combinations that are polymorphic within a
CC population of cells, such as the rearranged genes for Ig or TCR V
CC regions. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 222 AA;
    Query Match      84.7%; Score 538; DB 2; Length 222;
    Best Local Similarity 86.0%; Pred. No. 5.9e-42;
    Matches 104; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

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```

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHWRQPPGKGLEWLGVIWGGSTNN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTIVGAHWVRQPPGKGLEWLGVIWAGGSTNN 60

QY 61 SALMSRLSISKDNKSKQVFLKMNLSIQDQDTAMYYCARDSTMITAYAMDYWGQGTIVTVS 120
Db 61 SALMSRLSISKDNKSKQVFLKMNLSIQDQDTAMYYCARDRGA-----YWGQGTIVTVS 112

QY 121 S 121
Db 113 A 113

```

```

RESULT 8
AAR32840
ID AAR32840 standard; protein; 235 AA.
XX
AC AAR32840;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1993 (first entry)
XX
DE VH NQ2/12.4-Vk NQ10/12.5 linked peptide sequences.
XX
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazalone; hybridoma;
KW NQ2/12.4; NQ10/12.5.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..113
FT Peptide /label= VH_NQ2/12.4
FT Peptide 114..127
FT Region /note= "Linker peptide"
FT Region 128..235
FT /label= Vkappa_NQ2/12.4
XX
PN WO9303151-A1.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-GB001483.
XX
PR 10-AUG-1991; 91GB-00017352.
PR 11-JUN-1992; 92GB-00012419.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Embleton MJ, Gorochov G, Jones PT, Winter GP;
XX
XX WPI; 1993-076508/09.
DR N-PSDB; AAQ37459.
XX
PT Treatment of cell populations, partic. hybridomas - to link together
PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
XX Disclosure; Fig 2; 72pp; English.
PS

```

XX The sequences given in AAR32840-43 show the mature heavy chain VH domains
 CC and the VK light chain genes of the antiphenylloxazolone hybridomas
 CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
 CC cell PCR. The cDNA encoding these peptides was synthesised using forward
 CC primers annealing to the Ck gene and the JH segment, followed by assembly
 CC with linker primers. VH back primers based on the VH3 leader sequence and
 CC a forward Ck primer nested in respect to the primer used for cDNA. The
 CC assembled product within the cells is then amplified with nested primers
 CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
 CC In-cell PCR may be used to determine gene linkage analysis, particularly
 CC for the cloning of gene combinations that are polymorphic within a
 CC population of cells, such as the rearranged genes for Ig or TCR V
 CC regions. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 235 AA;

Query Match 84.7%; Score 538; DB 2; Length 235;
 Best Local Similarity 86.0%; Pred. No. 6.3e-42;
 Matches 104; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRPPGKGLWLGVIWGGSTNNY 60
 DB |||||
 QY 1 QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHVRPPGKGLWLGVIWAGGSTNNY 60
 DB |||||
 QY 61 SALMSRLSISKDQSKSQVFLKWNLSLQDDTAMYYCARDSMTITAYADYWGQGTITVS 120
 DB |||||
 QY 61 SALMSRLSISKDQSKSQVFLKWNLSLQDDTAMYYCARDSMTITAYADYWGQGTITVS 112

QY 121 S 121
 DB 113 A 113

RESULT 9
 AAG66520
 ID AAG66520 standard; protein; 142 AA.

AC AAG66520;

XX 22-OCT-2001 (first entry)

XX Mouse antibody 26 heavy chain variable region.

XX Mouse; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
 KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
 KW T cell; humanised antibody; autoimmune disorder; graft rejection;
 KW allergy; antibody 26; heavy chain variable region; VH.

XX Mus musculus.

XX WO200154732-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002653.

XX 27-JAN-2000; 2000US-0178473P.

XX (GEMY) GENETICS INST INC.

XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;

XX O'hara D, Hinton P, Tsurushita N;

XX WPI; 2001-493195/52.

XX N-PSDB; AAH76438.

XX Novel antibody-toxic group conjugate comprising an antibody that
 PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response.

XX Example 7; Page 84; 123pp; English.

XX The invention relates to an antibody-toxic group conjugate comprising an
 CC antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is preferably
 CC human cytotoxic T lymphocyte associated antigen 4 (CTLA4). The antibody
 CC of the invention is a humanised anti-CTLA4 antibody comprising a sequence
 CC of 128 or 142 amino acids fully defined in the specification. The
 CC antibody-toxic group conjugate is useful for modulating the immune
 CC response in a subject suffering from a disorder or condition such as
 CC autoimmune disorder, immune response to a graft, allergic response or an
 CC immune response to a therapeutic protein. The antibody is also useful for
 CC research purposes, e.g., in staining and isolating CTLA4-bearing cells.
 CC The antibody is also useful for T-cell typing, for isolating specific IL-
 CC 2 receptor-bearing cells or fragments of the receptor, for vaccine
 CC preparation, and for determining the effectiveness of an agent to down-
 CC regulate CTLA4 activity. The present sequence is the heavy chain variable
 CC region of mouse antibody 26. It was used in the construction of the
 CC humanised anti-CTLA4 antibody of the invention
 XX Sequence 142 AA;

Query Match 84.6%; Score 537; DB 4; Length 142;

Best Local Similarity 84.6%; Pred. No. 4.5e-42;
 Matches 104; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRPPGKGLWLGVIWGGSTNNY 60
 DB |||||
 QY 20 QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHVRPPGKGLWLGVIWAGGTNNY 79
 DB |||||
 QY 61 SALMSRLSISKDQSKSQVFLKWNLSLQDDTAMYYCAR--DRSTMITYADYWGQGTITV 118
 DB |||||
 QY 80 SALMSRLSISKDQSKSQVFLKWNLSLQDDTAMYYCARGPPEHAMKRGYADYWGQGTSVI 139

QY 119 VSS 121

DB 140 VSS 142

RESULT 10

AAV49218
 ID AAY49218 standard; protein; 119 AA.

XX AAY49218;

XX 07-FEB-2000 (first entry)

XX Heavy chain variable region consensus sequence.

XX Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;
 KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
 KW tumor-associated antigen.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 99..102
 FT /note= "residues Xaa are unspecified"

XX US5977316-A.

XX 02-NOV-1999.

XX 16-JAN-1996; 96US-00591196.

XX 17-JAN-1995; 95US-00372676.

XX (KENT) UNIV KENTUCKY.

XX Poon KA, Chatterjee SK, Chatterjee M;

XX WPI; 1996-354530/35.

XX Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)

PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma.

PS Disclosure; Fig 3C; 74pp; English.

XX The invention provides a monoclonal antibody (MAb) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2-associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the heavy chain variable region consensus sequence

XX Sequence 119 AA;

Query Match 84.3%; Score 535; DB 2; Length 119;
Best Local Similarity 86.0%; Pred. No. 5.6e-42;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLVWIGVWGSGTNYN 60
DB 1 QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHVRQPPGKGLVWIGVWGSGTNYN 60
QY 61 SALMSRLSISKDNSKQVFLKMNLSIQTDITAMYYCARDSTMITAYAMYDYGQGTSTVTS 120
DB 61 SALKSRLSISKDNSKQVFLKMNLSIQTDITARYYCAREXXX--XYIAMDYGQGTSTVTS 118
QY 121 S 121
DB 119 S 119

RESULT 11

ID ADA14778
AC ADA14778 standard; peptide; 119 AA.

XX ADA14778;

DT 06-NOV-2003 (first entry)

DE Peptide from antibody heavy chain resembling 1A7 #7.

XX heavy chain variable region; mouse; ganglioside GD2-associated tumour; melanoma; antibody; anti-idiotypic; monoclonal antibody; 1A7; neuroblastoma; glioma; sarcoma; small cell lung cancer.

OS Mus sp.

XX US6509016-B1.

PN 21-JAN-2003.

XX 15-APR-1999; 99US-00293533.

XX 17-JAN-1995; 95US-00372676.

PR 16-JAN-1996; 96US-00591196.

PR 21-NOV-1996; 96US-00752844.

XX (KENT) UNIV KENTUCKY.

XX Chatterjee M, Foon KA, Chatterjee SK;

PI WPI; 2003-401117/38.

XX Delaying recurrence and/or development of ganglioside GD2-associated tumor in individual, by administering antibody containing light and heavy chain variable region sequences contained in sequence of specified amino acids.

PS Example 2; Fig 3; 82pp; English.

XX

CC The invention relates to the recurrence and/or development of a ganglioside GD2-associated tumour, e.g. melanoma, in an individual which is delayed by administration of an antibody comprising light and heavy chain variable region sequences of the anti-idiotypic monoclonal antibody 1A7. The antibody is used for delaying recurrence and/or development of GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or small cell lung cancer, in individual, and for treating individual with GD2-associated tumour. The present sequence is a unique peptide region from an antibody sequence resembling the anti-idiotypic antibody 1A7 heavy chain.

CC Sequence 119 AA;

Query Match 84.3%; Score 535; DB 6; Length 119;

Best Local Similarity 86.0%; Pred. No. 5.6e-42;

Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLVWIGVWGSGTNYN 60

DB 1 QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHVRQPPGKGLVWIGVWGSGTNYN 60

QY 61 SALMSRLSISKDNSKQVFLKMNLSIQTDITAMYYCARDSTMITAYAMYDYGQGTSTVTS 120

DB 61 SALKSRLSISKDNSKQVFLKMNLSIQTDITARYYCAREXXX--XYIAMDYGQGTSTVTS 118

QY 121 S 121

DB 119 S 119

RESULT 12

ID ADC35320 standard; protein; 119 AA.

XX ADC35320;

XX 18-DEC-2003 (first entry)

DE Anti-idiotypic antibody VH region consensus sequence.

XX Mouse; monoclonal antibody; 1A7; anti-idiotypic antibody; ganglioside GD2; cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour; antibody; variable region; VH; VI; glioma; soft tissue sarcoma; vaccine.

OS Synthetic.

OS Mus sp.

XX US2003114398-A1.

XX 19-JUN-2003.

XX 21-MAY-2002; 2002US-00153401.

XX 17-JAN-1995; 95US-00372676.

PR 16-JAN-1996; 96US-00591196.

PR 15-APR-1999; 99US-00293533.

XX (CHAT/) CHATTERJEE M.

PA (FOON/) FOON K A.

PA (CHAT/) CHATTERJEE S K.

XX Chatterjee M, Foon KA, Chatterjee SK;

XX WPI; 2003-810913/76.

XX Novel anti-idiotypic monoclonal antibody 1A7, that is capable of recruiting a tumor-specific response against glycosphingolipid GD2, useful for treating a GD2-associated disease e.g., melanoma, glioma, soft tissue sarcoma.

PS Example 2; SEQ ID NO 16; 84pp; English.

CC The invention relates to a monoclonal antibody 1A7 (an anti-idiotypic
 CC antibody eliciting an anti-GD2(ganglioside) response). Also included are
 CC an antibody producing cell deposited under ATCC Accession No. HB-11786
 CC (or its progeny), a polynucleotide comprising a sequence encoding a
 CC polypeptide with immunological activity of 1A7 (where the polypeptide
 CC comprises at least 5 consecutive amino acids from a variable region of
 CC 1A7), an isolated polynucleotide comprising a region of at least 20
 CC consecutive nucleotides that is capable of forming a stable duplex with a
 CC polynucleotide encoding the light or heavy chain variable region of 1A7
 CC under conditions where the region does not form a stable hybrid with a
 CC polynucleotide consisting of a variable region encoding sequence
 CC appearing as ADC35321 - ADC35370, a host cell comprising the
 CC polynucleotide, a fusion polypeptide comprising 1A7, a humanised antibody
 CC comprising 5 consecutive amino acids from the 1A7 variable regions and a
 CC vaccine comprising the antibodies. The antibodies are useful for
 CC eliciting an immune response in an individual, and for treating a GD2-
 CC associated disease in an individual. The GD2-associated diseases is
 CC chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and
 CC small cell carcinoma. The individual has a clinically detectable tumour,
 CC and the method is for palliating the GD2-associated disease. 1A7 is
 CC preferably useful for treating a tumour that was previously detected in
 CC the individual and has been treated and is clinically undetectable at the
 CC time of the administering of 1A7, or for reducing the risk of recurrence
 CC of a clinically detectable tumour. 1A7 and the humanised antibody are
 CC useful for detecting the presence of an anti-GD2 antibody bound to a
 CC tumour cell. The present sequence represents a consensus sequence for the
 CC light or heavy chain variable region of monoclonal antibody 1A7.

XX
 SQ Sequence 119 AA;

Query Match 84.3%; Score 535; DB 7; Length 119;
 Best Local Similarity 86.0%; Pred. No. 5 6e-42;
 Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSSQSLTCTVSGISLNRYGVHWRPQPGKLEWLVGVITGGSTNN 60
 DB 1 QVQLKESGPGLVAPSSQSLTCTVSGISLNRYGVHWRPQPGKLEWLVGVITGGSTNN 60

QY 61 SALKSRSLTSISKDMSKQVFLKMSLQTDITAMYYCARDSTMTAYAMDYWGQGTSTVTS 120
 DB 61 SALKSRSLTSISKDMSKQVFLKMSLQTDITAMYYCARDSTMTAYAMDYWGQGTSTVTS 118

QY 121 S 121

DB 119 S 119

RESULT 13

AAW07438
 ID AAW07438 standard; protein; 123 AA.

XX AAW07438;

XX 12-AUG-1997 (first entry)

XX Anti-DNA antibody 11f8 group heavy chain variable region.

XX Heavy chain; variable region; anti-DNA; monoclonal; antibody; 11f8 group;
 KW hairpin; diagnosis; inflammatory glomerulonephritis;
 KW systemic lupus erythematosus; screening; treatment; prevention; SLE;
 KW disease; consensus; putative.

XX Synthetic.

XX Key Location/Qualifiers
 FH Region 1..30
 FT /label= framework_I
 FT Region 31..35
 FT /label= CDR_I
 FT Region 36..49
 FT /label= framework_II
 FT Region 50..66
 FT /label= CDR_II

FT Region 67..98
 FT /label= framework_III
 FT Region 99..112
 FT /label= CDR_III
 FT Region 113..123
 FT /label= J_region

XX WO9636361-A1.

XX 21-NOV-1996.

XX 16-MAY-1996; 96WO-US007113.

XX 18-MAY-1995; 95US-00443540.

XX (UNMI) UNIV MICHIGAN.

XX Glick GD, Swanson PC;

XX WPI; 1997-011854/01.

XX Anti-DNA antibody which specifically binds DNA hairpin - useful to
 PT develop prods. for diagnosis and treatment of disorders, e.g.
 PT glomerulonephritis or systemic lupus erythematosus.

PS Example; Fig 9; 102pp; English.

XX The present sequence is the heavy chain variable region of the group 11f8
 CC putative consensus anti-DNA monoclonal antibody (Mab), which has a high
 CC affinity for single stranded DNA, low or no affinity for double stranded
 CC DNA and specifically binds a DNA hairpin. The Mab can be used to diagnose
 CC disorders associated with the pathological complexation of DNA, e.g.
 CC inflammatory glomerulonephritis and systemic lupus erythematosus. It can
 CC also be used to generate reagents to screen for pharmaceutical agents,
 CC and treat and/or prevent an above disorder. The sequence was derived by
 CC aligning homologous anti-DNA MAB, whose sequences have been published, as
 CC well as several MAB of other specificities obtained from a database
 CC search

XX Sequence 123 AA;

Query Match 84.1%; Score 534; DB 2; Length 123;

Best Local Similarity 87.0%; Pred. No. 7.2e-42;
 Matches 107; Conservative 2; Mismatches 12; Indels 2; Gaps 2;

QY 1 QVQLQESGPGLVAPSSQSLTCTVSGISLNRYGVHWRPQPGKLEWLVGVITGGSTNY 59
 DB 1 QVQLKESGPGLVAPSSQSLTCTVSGISLNRYGVHWRPQPGKLEWLVGVITGGSTNY 60

QY 60 NSALMSRLTSISKDMSKQVFLKMSLQTDITAMYYCARDSTMTAYAMDYWGQGTSTV 118
 DB 61 NSALMSRLTSISKDMSKQVFLKMSLQTDITAMYYCARDSTMTAYAMDYWGQGTSTV 120

QY 119 VSS 121

DB 121 VSS 123

RESULT 14

AAR32569
 ID AAR32569 standard; protein; 269 AA.

XX AAR32569;

XX 25-MAR-2003 (revised)

DT 08-JUN-1993 (first entry)

XX Fusion protein encoded by Ox VH-hinge-VL insert.

XX Spacer peptide; secretable; single chain; antibody; recombinant; scAb;
 KW rDNA; linker; Bos taurus.

XX Synthetic.


```

XX Key
FH Region
FT 1. .22
FT /note= "SS"
FT Region
FT 23.135
FT /note= "VH"
FT Region
FT 136.163
FT /note= "CBHI hinge"
FT Region
FT 164.277
FT /note= "VL"
XX
XX FI9103434-A.
XX
XX 17-JAN-1992.
XX
XX 16-JUL-1991; 91FI-00913434.
XX
XX 16-JUL-1990; 90US-00552751.
XX
XX (TERE-) TECH RES CENT FINLA.
XX
XX WPI; 1992-134225/17.
XX N-PSDB; AAQ36982.
XX
XX Sepd. recombinant fusion proteins.
XX
XX Example; Fig 4; 56pp; English.
XX
XX The sequence is that of the fusion protein encoded by the Ox VH-CBHI
XX hinge-VL insert which was used as part of a method for cloning
XX secretable, biologically active single chain antibodies (scAbs) and other
XX secretable fusion proteins having at least 2 distinct functional proteins
XX or domains. NOTE: This patent has been indexed using data derived from
XX patent WO9302198-A. (First Major Country Equivalent). (Updated on 25-MAR-
XX 2003 to correct PF field.)
XX
XX Sequence 269 AA;
XX
Query Match 84.1%; Score 534; DB 2; Length 269;
Best Local Similarity 85.1%; Pred. No. 1.7e-41;
Matches 103; Conservative 2; Mismatches 8; Indels 8; Gaps 1;
QY 1 QVLOESGPGGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGTGSTNYN 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 QVQLKESGPGGLVAPQSLSITCTASGFSLTSGVHVRQPPGKGLWLGVIWAGGSTNYN 82
QY 61 SALMSRLSISKDNKSQVFLKXNSLQTDITAMYCARDSTMITAYAMDYWGQGTITVTS 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 SALMSRLSISKDNKSQVFLKXNSLQTDITAMYCARDSTMITAYAMDYWGQGTITVTS 134
QY 121 S 121
Db 135 A 135
XX
RESULT 15
AAB49243
ID AAB49243 standard; protein; 476 AA.
XX
XX AAB49243;
XX
XX 15-MAR-2001 (first entry)
XX
XX Chimeric 4H6 anti-DR4 antibody heavy chain protein.
XX
XX Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;
XX autoimmune.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO2000073349-A1.
XX
PD 07-DEC-2000.
XX
XX 25-MAY-2000; 2000WO-US014599.
XX
XX 28-MAY-1999; 99US-00322875.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;
XX WPI; 2001-041145/05.
XX
XX Novel anti-death receptor 4 antibodies useful for treating cancer and
XX immune related disorders such as rheumatoid arthritis, sjogren's
XX syndrome, Grave's disease and diabetes mellitus.
XX
XX Claim 16; Fig 18; 126pp; English.
XX
XX The present invention relates to an anti-Death receptor 4 (DR4) antibody.
XX The antibodies of the invention are useful for inducing apoptosis in
XX mammalian cancer cells such as colon cancer cells and for treating an
XX immune-related disease in a mammal such as arthritis and autoimmune
XX disease
XX
XX Sequence 476 AA;
XX
Query Match 83.8%; Score 532; DB 4; Length 476;
Best Local Similarity 81.0%; Pred. No. 5e-41;
Matches 102; Conservative 11; Mismatches 7; Indels 6; Gaps 1;
QY 2 VQLOESGPGGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLWLGVIWGTGSTNYN 61
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 VQLKESGPGGLVAPQSLSITCTVSGFSLTSGVHVRQPPGKGLWLGVIWAGGSTNYN 80
QY 62 ALMSRLSISKDNKSQVFLKXNSLQTDITAMYCARDSTMITAYAMDYWGQGT 115
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 ALMSRLSISKDNKSQVFLKXNSLQTDITAMYCARDSTMITAYAMDYWGQGT 140
QY 116 TVTVSS 121
Db 141 SVTVSS 146
XX
Search completed: October 13, 2004, 12:55:11
Job time : 115.933 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:59:19 ; Search time 87.2208 Seconds
(without alignments)
447.653 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPSSLSI.....MITAYAMDYWGQTTVTYSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	87.7	113	16	US-10-803-622-218
2	557	87.7	113	16	US-10-803-622-218
3	546	86.0	253	15	US-10-239-656-63
4	537	84.6	142	9	US-09-772-103-4
5	535	84.3	119	14	US-10-153-401-16
6	532	83.8	476	16	US-10-660-128-12
7	531.5	83.7	140	8	US-08-973-518-4
8	531.5	83.7	140	9	US-09-007-093-4
9	531.5	83.7	140	14	US-10-428-754-4
10	531	83.6	119	14	US-10-232-187-2
11	526	82.8	119	15	US-10-239-656-23
12	523	82.4	119	14	US-10-144-644-15
13	523	82.4	119	16	US-10-700-740-15
14	521.5	82.1	112	9	US-09-824-286-3
					Sequence 218, App
					Sequence 218, App
					Sequence 63, Appl
					Sequence 4, Appl
					Sequence 16, Appl
					Sequence 12, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 2, Appl
					Sequence 23, Appl
					Sequence 15, Appl
					Sequence 3, Appl

15	521	82.0	121	14	US-10-207-655-252	Sequence 252, App
16	521	82.0	271	14	US-10-207-655-254	Sequence 254, App
17	521	82.0	556	14	US-10-207-655-268	Sequence 268, App
18	517.5	81.5	116	14	US-10-169-351-108	Sequence 108, App
19	517.5	81.5	241	16	US-10-803-622-187	Sequence 187, App
20	517.5	81.5	241	16	US-10-803-622-187	Sequence 187, App
21	517.5	81.5	272	16	US-10-803-622-183	Sequence 183, App
22	517.5	81.5	272	16	US-10-803-622-183	Sequence 183, App
23	515.5	81.2	120	14	US-10-194-975-112	Sequence 112, App
24	514.5	81.0	116	14	US-10-194-975-100	Sequence 100, App
25	510.5	80.4	135	16	US-10-351-748-31	Sequence 31, Appl
26	510.5	80.4	135	17	US-10-351-748-31	Sequence 31, Appl
27	508.5	80.1	333	14	US-10-059-261-61	Sequence 61, Appl
28	505.5	79.6	139	8	US-08-779-784-37	Sequence 37, Appl
29	505.5	79.6	241	15	US-10-353-721-13	Sequence 13, Appl
30	503	79.2	249	9	US-09-730-374-3	Sequence 3, Appl
31	503	79.2	249	16	US-10-704-206-3	Sequence 3, Appl
32	502	79.1	121	11	US-09-842-776A-52	Sequence 52, Appl
33	501.5	79.0	116	15	US-10-435-299-4	Sequence 4, Appl
34	501.5	79.0	118	14	US-10-056-052-16	Sequence 16, Appl
35	500	78.7	121	14	US-10-056-052-12	Sequence 12, Appl
36	494.5	77.9	119	13	US-10-140-555-2	Sequence 2, Appl
37	494.5	77.9	139	9	US-09-881-823-4	Sequence 4, Appl
38	493.5	77.7	120	16	US-10-697-339-5	Sequence 5, Appl
39	491.5	77.4	135	14	US-10-010-729-68	Sequence 68, Appl
40	490.5	77.2	116	16	US-10-682-845-53	Sequence 53, Appl
41	490.5	77.2	492	16	US-10-682-845-59	Sequence 59, Appl
42	490.5	77.2	492	16	US-10-682-845-61	Sequence 61, Appl
43	490.5	77.2	492	16	US-10-682-845-65	Sequence 65, Appl
44	490.5	77.2	492	16	US-10-682-845-65	Sequence 65, Appl
45	490.5	77.2	492	16	US-10-682-845-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-803-622-218
; Sequence 218, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134

; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-218

Query Match 87.7%; Score 557; DB 16; Length 113;
Best Local Similarity 89.3%; Pred. No. 2e-46;
Matches 108; Conservative 0; Mismatches 5; Indels 8; Gaps 1;
QY 1 QVQLQESGFLVAPSGQSLSITCTVSGISLNRYGVHWVRPPGKGLWLVITGGSTNYN 60
Db 1 QVQLQESGFLVAPSGQSLSITCTVSGFSLTSYGVHWVRPPGKGLWLVITGGSTNYN 60
QY 61 SALMSRLSISKNSKSOVFLKMNLSQTDDTAMYYCARDRSTMITAYAMYWGQGTITVTS 120
Db 61 SALMSRLSISKNSKSOVFLKMNLSQTDDTAMYYCARDRSTMITAYAMYWGQGTITVTS 112
QY 121 S 121
Db 113 S 113

RESULT 2

US-10-803-653-218
; Sequence 218, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Medical Research Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893

; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-218

Query Match 87.7%; Score 557; DB 16; Length 113;
Best Local Similarity 89.3%; Pred. No. 2e-46;
Matches 108; Conservative 0; Mismatches 5; Indels 8; Gaps 1;
QY 1 QVQLQESGFLVAPSGQSLSITCTVSGISLNRYGVHWVRPPGKGLWLVITGGSTNYN 60
Db 1 QVQLQESGFLVAPSGQSLSITCTVSGFSLTSYGVHWVRPPGKGLWLVITGGSTNYN 60
QY 61 SALMSRLSISKNSKSOVFLKMNLSQTDDTAMYYCARDRSTMITAYAMYWGQGTITVTS 120
Db 61 SALMSRLSISKNSKSOVFLKMNLSQTDDTAMYYCARDRSTMITAYAMYWGQGTITVTS 112
QY 121 S 121
Db 113 S 113

RESULT 3

US-10-239-656-63
; Sequence 63, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-3 single
; OTHER INFORMATION: Chain Fv
US-10-239-656-63

Query Match 86.0%; Score 546; DB 15; Length 253;
Best Local Similarity 88.5%; Pred. No. 5.7e-45;
Matches 108; Conservative 2; Mismatches 8; Indels 4; Gaps 2;
QY 1 QVQLQESGFLVAPSGQSLSITCTVSGISLNRYGVHWVRPPGKGLWLVITGGSTNY 59
Db 1 EVQLLEESGFLVAPSGQSLSITCTVSGFSLTSYGVHWVRPPGKGLWLVITGGSTNY 60
QY 60 NSALMSRLSISKNSKSOVFLKMNLSQTDDTAMYYCARDRSTMITAYAMYWGQGTITV 119
Db 61 NSALMSRLSISKNSKSOVFLKMNLSQTDDTAMYYCARDRSTMITAYAMYWGQGTITV 117
QY 120 SS 121

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Db      118 SS 119
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RESULT 4
US-09-772-103-4
; Sequence 4, Application US/09772103
; Publication No. US20020039581A1
; GENERAL INFORMATION:
; APPLICANT: Carreno, Beatriz M.
; APPLICANT: Wood, Clive
; APPLICANT: Turner, Katherine
; APPLICANT: Collins, Mary
; APPLICANT: Gray, Gary S.
; APPLICANT: Morris, Donna
; APPLICANT: O'Hara, Denise
; APPLICANT: Hinton, Paul
; APPLICANT: Tsurushita, Naoya
; TITLE OF INVENTION: ANTIBODIES AGAINST CTLA4 AND USES THEREFOR
; FILE REFERENCE: GNN-009CP
; CURRENT APPLICATION NUMBER: US/09/772,103
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/178,473
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-772-103-4

Query Match      84.6%; Score 537; DB 9; Length 142;
Best Local Similarity 84.6%; Pred. No. 2.3e-44;
Matches 104; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY      1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLWGLVITGGSTNN 60
Db      20 QVQLKESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLWGLVITGGSTNN 79
QY      61 SALMSRLSISKDMSKQVFLKMSLSQTDITAMYYCAR--DRSTMITAYMDYWGQGTIVT 118
Db      80 SALMSRLSISKDMSKQVFLKMSLSQTDITAMYYCAR--DRSTMITAYMDYWGQGTIVT 118
QY      119 VSS 121
Db      140 VSS 142

RESULT 5
US-10-153-401-16
; Sequence 16, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-153-401-16

Query Match      84.3%; Score 535; DB 14; Length 119;
Best Local Similarity 86.0%; Pred. No. 2.9e-44;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY      1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLWGLVITGGSTNN 60
Db      1 QVQLKESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLWGLVITGGSTNN 60
QY      61 SALMSRLSISKDMSKQVFLKMSLSQTDITAMYYCARDSMTITAYMDYWGQGTIVTS 120
Db      61 SALMSRLSISKDMSKQVFLKMSLSQTDITARIYCARXXX--XYAYMDYWGQGTIVTS 118
QY      121 S 121
Db      119 S 119

RESULT 6
US-10-660-128-12
; Sequence 12, Application US/10660128
; Publication No. US20040120947A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Dodge, Kelly
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: DR4 Antibodies and Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/660,128
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/09/584,166
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 09/322,875
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/237,299
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: US 60/072,481
; PRIOR FILING DATE: 1998-01-26
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 12
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.

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FEATURE:

NAME/KEY: Misc_feature
LOCATION: 20
OTHER INFORMATION: Xaa may be glutamine or glutamic acid
US-10-660-128-12

Query Match 83.8%; Score 532; DB 16; Length 476;
Best Local Similarity 81.0%; Pred. No. 2.7e-43;
Matches 102; Conservative 11; Mismatches 7; Indels 6; Gaps 1;

QY 2 VQLQESGPGGLVAPSQSLTCTVSGISLNRVGVHVRQPPGKGLWLVGVIWGGSTNNYS 61
DB 21 VQLQESGPGGLVAPSQSLTCTVSGISLNRVGVHVRQPPGKGLWLVGVIWGGSTNNYS 80
QY 62 ALMSRLSISKDNKSKQVFLKMNLSLQDDTAMYYCARD-----RSTMITAYANDYWGQGT 115
DB 81 ALMSRLSISKDNKSKQVFLKMNLSLQDDTAMYYCARDGEFDYGGSSLLYHSMNFWGQGT 140
QY 116 FTVVSS 121
DB 141 SVTVSS 146

RESULT 7

US-08-973-518-4
Sequence 4, Application US/08973518
Publication No. US20010014327A1
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,518
FILING DATE: 07-APR-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-973-518-4
Query Match 83.7%; Score 531.5; DB 8; Length 140;
Best Local Similarity 85.1%; Pred. No. 7.6e-44;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 VQLQESGPGGLVAPSQSLTCTVSGISLNRVGVHVRQPPGKGLWLVGVIWGGSTNNYN 60

DB 21 VQLQESGPGGLVAPSQSLTCTVSGISLNRVGVHVRQPPGKGLWLVGVIWGGSTNNYN 80
QY 61 SALMSRLSISKDNKSKQVFLKMNLSLQDDTAMYYCARDSTMTITAYANDYWGQGTTVTVS 120
DB 81 SALMSRLSISKDNKSKQVFLKMNLSLQDDTAMYYCARDSTMTITAYANDYWGQGTTVTVS 139
QY 121 S 121
DB 140 S 140

RESULT 8

US-09-007-093-4
Sequence 4, Application US/09007093
Patent No. US20020025315A1
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/483,576
APPLICATION NUMBER: 07-JUN-1995
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-007-093-4
Query Match 83.7%; Score 531.5; DB 9; Length 140;
Best Local Similarity 85.1%; Pred. No. 7.6e-44;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 VQLQESGPGGLVAPSQSLTCTVSGISLNRVGVHVRQPPGKGLWLVGVIWGGSTNNYN 60
DB 21 VQLQESGPGGLVAPSQSLTCTVSGISLNRVGVHVRQPPGKGLWLVGVIWGGSTNNYN 80
QY 61 SALMSRLSISKDNKSKQVFLKMNLSLQDDTAMYYCARDSTMTITAYANDYWGQGTTVTVS 120
DB 81 SALMSRLSISKDNKSKQVFLKMNLSLQDDTAMYYCARDSTMTITAYANDYWGQGTTVTVS 139
QY 121 S 121
DB 140 S 140

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RESULT 9
US-10-428-754-4
; Sequence 4, Application US/10428754
; Publication No. US20030228304A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; Barber, Brian H
; Cates, George A
; Caterini, Judith E
; Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/428,754
; FILING DATE: 05-May-2003
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 10/428,754
; FILING DATE: 05-MAY-2003
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-1065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-428-754-4
Query Match 83.7%; Score 531.5; DB 14; Length 140;
Best Local Similarity 85.1%; Pred. No. 7.6e-44;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVAPSGQSLSITCTVSGISLNRYGVHWVRQPPGKGLWLGVIWGTGSTNN 60
Db 21 QVQLKESGPGLVAPSGQSLSITCTVSGISLNRYGVHWVRQPPGKGLWLGVIWGTGSTNN 80
QY 61 SALMSRLSISKDNKSQVFLKMNLSLQDQDTTAMYYCARDRSTMTAYANDYWGQGTITVTS 120
Db 81 SALMSRLSISKDNFKSQVFLKMNLSLQDQDTTAMYYCARDYGVV-HYAMDYWGQGTITVTS 139
QY 121 S 121
Db 140 S 140
RESULT 10
US-10-232-187-2
; Sequence 2, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
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; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-232-187-2
Query Match 83.6%; Score 531; DB 14; Length 119;
Best Local Similarity 86.0%; Pred. No. 7.1e-44;
Matches 104; Conservative 7; Mismatches 8; Indels 2; Gaps 2;
QY 1 QVQLQESGPGLVAPSGQSLSITCTVSGISLNRYGVHWVRQPPGKGLWLGVIWGTGSTNN 60
Db 1 QVQLKESGPGLVAPSGQSLSITCTVSGISLNRYGVHWVRQPPGKGLWLGVIWGTGSTNN 59
QY 61 SALMSRLSISKDNKSQVFLKMNLSLQDQDTTAMYYCARDRSTMTAYANDYWGQGTITVTS 120
Db 60 SALMSRLSISKDNKSQVFLKMNLSLQDQDTTAMYYCARDRSTMTAYANDYWGQGTITVTS 118
QY 121 S 121
Db 119 S 119
RESULT 11
US-10-239-656-23
; Sequence 23, Application US/10239656
; Publication No. US2004003839A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D
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OTHER INFORMATION: hybridoma 6H7E7 variable heavy chain
US-10-239-656-23

Query Match 82.8%; Score 526; DB 15; Length 119;
Best Local Similarity 86.0%; Pred. No. 2.2e-43;
Matches 104; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNN 60
DB 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNN 60

QY 61 SALMSRLSISKDMSKQVFLKNSLQTDITAMYYCARDSTMTITAYAMDYWGQGITVTVS 120
DB 61 SALMSRLSISKDMSKQVFLKNSLQTDITAMYYCARDSTMTITAYAMDYWGQGITVTVS 118

QY 121 S 121
DB 119 S 119

RESULT 12
US-10-144-644-15
Sequence 15, Application US/10144644
Publication No. US20030059429A1
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-144-644-15

Query Match 82.4%; Score 523; DB 14; Length 119;
Best Local Similarity 82.6%; Pred. No. 4.2e-43;
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNN 60
DB 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNN 60

QY 61 SALMSRLSISKDMSKQVFLKNSLQTDITAMYYCARDSTMTITAYAMDYWGQGITVTVS 120
DB 61 SALMSRLSISKDMSKQVFLKNSLQTDITAMYYCARDSTMTITAYAMDYWGQGITVTVS 118

QY 121 S 121
DB 119 S 119

RESULT 13
US-10-700-740-15
Sequence 15, Application US/10700740
Publication No. US20040156850A1
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-Nov-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-700-740-15

Query Match      82.4%; Score 523; DB 16; Length 119;
Best Local Similarity 82.6%; Pred. No. 4.2e-43;
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLVGLVITGGSTNNYN 60
Db 1 QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHWVRQPPGKGLVGLVITWASGTDYN 60

QY 61 SALMSRLSISKDNSKQVFLKMNLSIQDDTAMYYCARDSTMTITAYAMYDYGQGTITVS 120
Db 61 SALMSRLSISKDNSKQVFLKMNLSIQDDTAMYYCARDPSSL--LRLDYWGQGTITLVS 118

QY 121 S 121
Db 119 S 119

RESULT 14
US-09-824-286-3
; Sequence 3, Application US/09824286
; Patent No. US20020028202A1
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; Benjamin, Christopher D
; Hession, Catherine A
; Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,286
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-824-286-3
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Query Match 82.1%; Score 521.5; DB 9; Length 112;
Best Local Similarity 85.2%; Pred. No. 5.5e-43;

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Matches 98; Conservative 8; Mismatches 6; Indels 3; Gaps 1;

QY 4 LOESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLVGLVITGGSTNNYN 63
Db 1 LOESGPGLVAPQSLSITCTVSGFSLTSYGVHWVRQPPGKGLVGLVITWASGSTNNYN 60

QY 64 MSRLSISKDNSKQVFLKMNLSIQDDTAMYYCARDSTMTITAYAMYDYGQGTITVT 118
Db 61 MSRLNLRDNSKQVFLKMNLSIQDDTATYYCAREGSTV---DSMDYWGQGTITVT 112

RESULT 15
US-10-207-655-252
; Sequence 252, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 252
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-252
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Query Match 82.0%; Score 521; DB 14; Length 121;
Best Local Similarity 82.6%; Pred. No. 6.7e-43;
Matches 100; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHWVRQPPGKGLVGLVITGGSTNNYN 60
Db 1 QVQLKESGPGLVAPQSLSITCTVSGFSLTGYGVNWRQPPGKGLVGLVITWASGTDYN 60

QY 61 SALMSRLSISKDNSKQVFLKMNLSIQDDTAMYYCARDSTMTITAYAMYDYGQGTITVS 120
Db 61 SALMSRLSITKDNKSKQVFLKMNLSIQDDTARYICARDGYSNFHYVMDYWGQGTITVS 120

QY 121 S 121
Db 121 S 121
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Search completed: October 13, 2004, 13:15:28
Job time : 88.2208 secs

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Db 1 QVQLKESGFLVAPQSLSITCTVSGFSLTSGVHWVRQPPGKGLWLGVIWAGGSTNN 60
QY 61 SALMSRLSISKNSKQVFLKNSLQTDTTAMYYCARDRSTMTAYAMDYWGQTTVTS 120
Db 61 SALMSRLSISKNSKQVFLKNSLQTDTTAMYYCARDRGA-----YWGQTLTVTS 112
QY 121 S 121
Db 113 A 113
RESULT 2
US-08-190-199A-61
; Sequence 61, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-190-199A-61
Query Match 84.7%; Score 538; DB 2; Length 235;
Best Local Similarity 86.0%; Pred. No. 7.4e-48;
Matches 104; Conservative 2; Mismatches 7; Indels 8; Gaps 1;
QY 1 QVQLKESGFLVAPQSLSITCTVSGFSLTSGVHWVRQPPGKGLWLGVIWAGGSTNN 60
Db 1 QVQLKESGFLVAPQSLSITCTVSGFSLTSGVHWVRQPPGKGLWLGVIWAGGSTNN 60
QY 61 SALMSRLSISKNSKQVFLKNSLQTDTTAMYYCARDRSTMTAYAMDYWGQTTVTS 120
Db 61 SALMSRLSISKNSKQVFLKNSLQTDTTAMYYCARDRGA-----YWGQTLTVTS 112
QY 121 S 121
Db 113 A 113
RESULT 3

US-08-652-558-38
; Sequence 38, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-38
Query Match 84.3%; Score 535.5; DB 2; Length 120;
Best Local Similarity 86.0%; Pred. No. 5.9e-48;
Matches 104; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
QY 1 QVQLKESGFLVAPQSLSITCTVSGFSLTSGVHWVRQPPGKGLWLGVIWAGGSTNN 60
Db 1 QVQLKESGFLVAPQSLSITCTVSGFSLTSGVHWVRQPPGKGLWLGVIWAGGSTNN 60
QY 61 SALMSRLSISKNSKQVFLKNSLQTDTTAMYYCARDRSTMTAYAMDYWGQTTVTS 120
Db 61 SALMSRLSISKNSKQVFLKNSLQTDTTAMYYCARDRVT-ATLYAMDYWGQTSVTVS 119
QY 121 S 121
Db 120 S 120
RESULT 4
US-08-752-844-16
; Sequence 16, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD

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; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-591-196-16

Query Match      84.3%; Score 535; DB 2; Length 119;
Best Local Similarity 86.0%; Pred. No. 6.6e-48;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSSQSLISITCTVSGISLNRYGVHVRQPPKGLWLGVIWGTGSTNYN 60
Db 1 QVQLKESGPGLVAPSSQSLISITCTVSGFSLTSYGVHVRQPPKGLWLGVIWGDGSTNYN 60
QY 61 SALMSRLSISKDNKSQVFLKMNLSLQDDTAMYYCARDRSTMTAYAMDYWGQGTSTVTS 120
Db 61 SALKSRLSISKDNKSQVFLKMNLSLQDDTARYYCAREXXX--YYAMDYWGQGTSTVTS 118
QY 121 S 121
Db 119 S 119

RESULT 6
US-09-293-533-16
; Sequence 16, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141

; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-293-533-16

Query Match 84.3%; Score 535; DB 4; Length 119;
Best Local Similarity 86.0%; Pred. No. 6.e-48;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;
QY 1 QVQLQESGPGLVAPSSQSLITCTVSGISLNRYGVHWRQPPGKGLWLVGIWVGSTNN 60
DB 1 QVQLKESGPGLVAPSSQSLITCTVSGFSLTSYGVHWRQPPGKGLWLVGIWVGSTNN 60
QY 61 SALMSRLSISKNSKQVFLKNNLSLQDDTAMYYCARDRSTMITAYAMDYWGQGTIVTS 120
DB 61 SALKSRLSISKNSKQVFLKNNLSLQDDTARYYCAREXXX--XYAMDYWGQGTIVTS 118
QY 121 S 121
DB 119 S 119

RESULT 7
US-08-943-136-4
; Sequence 4, Application US/08943136
; Patent No. 6291208
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,136
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-943-136-4

Query Match 83.7%; Score 531.5; DB 3; Length 140;
Best Local Similarity 85.1%; Pred. No. 1.8e-47;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVAPSSQSLITCTVSGISLNRYGVHWRQPPGKGLWLVGIWVGSTNN 60
DB 21 QVQLKESGPGLVAPSSQSLITCTVSGFSLTSYGVHWRQPPGKGLWLVGIWVGSTNN 80
QY 61 SALMSRLSISKNSKQVFLKNNLSLQDDTAMYYCARDRSTMITAYAMDYWGQGTIVTS 120
DB 81 SALKSRLSISKNSKQVFLKNNLSLQDDTAMYYCARAYGDYV-HYAMDYWGQGTIVTS 139
QY 121 S 121
DB 140 S 140

RESULT 8
US-08-973-518-4
; Sequence 4, Application US/08973518
; Patent No. 6328962
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-973-518-4

Query Match 83.7%; Score 531.5; DB 3; Length 140;
Best Local Similarity 85.1%; Pred. No. 1.8e-47;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVAPSSQSLITCTVSGISLNRYGVHWRQPPGKGLWLVGIWVGSTNN 60
DB 21 QVQLKESGPGLVAPSSQSLITCTVSGFSLTSYGVHWRQPPGKGLWLVGIWVGSTNN 80
QY 61 SALMSRLSISKNSKQVFLKNNLSLQDDTAMYYCARDRSTMITAYAMDYWGQGTIVTS 120
DB 81 SALKSRLSISKNSKQVFLKNNLSLQDDTAMYYCARAYGDYV-HYAMDYWGQGTIVTS 139

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; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-67

Query Match      82.8%; Score 525.5; DB 3; Length 121;
Best Local Similarity 86.0%; Pred. No. 6.4e-47;
Matches 104; Conservative 2; Mismatches 14; Indels 1; Gaps 1

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Db 1 QVQLQESGPGVLVAPSSQSLTCTVSGIFSLTSYGIVHWVRPPKGLWLGVIWAGGSTNNY 60
Qy 61 SALMSRLSISKNSKSQVFLKNLSLOTDDTAMYYCARDRS-TMIATAYANDYWGQGTSTVTY 119
Db 61 SALMSRLSISKNSKSQVFLKNLSLOTDDTAMYYCAKHLPIYGNLYGYANDYWGQGTSTVTY 120
Qy 120 S 120
Db 121 S 121

RESULT 11
US-08-667-769A-15
; Sequence 15, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McWilliam, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,769A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082
; FILING DATE: 22-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:

; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-67

Query Match      83.4%; Score 529.5; DB 6; Length 242;
Best Local Similarity 85.8%; Pred. No. 5.7e-47;
Matches 103; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

Qy 2 VQLQESGPGLVAPSSQSLTCTVSGISLNRYGVHVRPDPKGLWLGVIWTGGSTNNYS 61
Db 124 VQLQESGPGVLVAPSSQSLTCTVSGIFSLTSYGIVHWVRPPKGLWLGVIWAGGSTNNYS 183
Qy 62 ALMSRLSISKNSKSQVFLKNLSLOTDDTAMYYCARDRSTMITAYANDYWGQGTSTVSS 121
Db 184 ALMSRLSISKNSKSQVFLKNLSLOTDDTAMYYCAK-LRIERIFYANDYWGQGTSTVSS 242

RESULT 10
US-08-881-037-67
; Sequence 67, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Gluck, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.

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RESULT 13
US-09-189-129-3
; Sequence 3, Application US/09189129
; Patent No. 6323027
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; APPLICANT: Benjamin, Christopher D
; APPLICANT: Hession, Catherine A
; APPLICANT: Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,129
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: A006 PCT CIP
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	68.0	235	3	US-09-171-945-17
2	445	66.0	215	6	Sequence 17, Appli
3	445	66.0	235	2	Patent No. 5455030
4	445	66.0	235	2	Sequence 5, Appli
5	445	66.0	235	4	Sequence 5, Appli
6	445	66.0	235	4	Sequence 5, Appli
7	444	65.9	255	3	Sequence 5, Appli
8	444	65.9	255	4	Sequence 5, Appli
9	443.5	65.8	213	2	Sequence 8, Appli
10	439	65.1	108	3	Sequence 4, Appli
11	427	63.4	256	4	Sequence 9, Appli
12	427	63.4	258	4	Sequence 2, Appli
					Sequence 4, Appli

13	426	63.2	270	2	US-08-652-507-2	Sequence 2, Appli
14	426	63.2	553	2	US-08-661-052-16	Sequence 16, Appli
15	426	63.2	553	3	US-09-188-082-16	Sequence 16, Appli
16	426	63.2	553	3	US-09-364-088-16	Sequence 16, Appli
17	426	63.2	553	3	US-09-102-716-16	Sequence 16, Appli
18	426	63.1	223	3	US-08-190-199A-63	Sequence 63, Appli
19	425	63.1	235	3	US-09-423-439-58	Sequence 58, Appli
20	425	63.1	235	4	US-09-011-789A-23	Sequence 23, Appli
21	425	63.1	236	2	US-08-190-199A-65	Sequence 65, Appli
22	424	62.9	222	2	US-08-190-199A-67	Sequence 67, Appli
23	424	62.9	235	2	US-08-190-199A-61	Sequence 61, Appli
24	420	62.3	106	2	US-08-956-047-33	Sequence 33, Appli
25	420	62.3	128	2	US-08-956-047-31	Sequence 31, Appli
26	420	62.3	240	2	US-08-956-047-25	Sequence 25, Appli
27	420	62.3	281	3	US-09-423-439-44	Sequence 44, Appli
28	420	62.3	666	3	US-09-423-439-51	Sequence 51, Appli
29	417	61.9	108	4	US-09-948-004-28	Sequence 28, Appli
30	417	61.9	495	4	US-09-948-004-18	Sequence 18, Appli
31	414	61.4	103	1	US-08-467-393-4	Sequence 4, Appli
32	414	61.4	144	4	US-08-318-786-29	Sequence 29, Appli
33	413	61.3	129	2	US-08-116-778E-2	Sequence 2, Appli
34	413	61.3	129	2	US-08-438-562-2	Sequence 2, Appli
35	413	61.3	129	2	US-08-483-528B-92	Sequence 92, Appli
36	413	61.3	242	2	US-08-553-497A-28	Sequence 28, Appli
37	410.5	60.9	107	1	US-07-942-245-3	Sequence 3, Appli
38	409.5	60.8	110	3	US-08-836-561-33	Sequence 33, Appli
39	409.5	60.8	110	4	US-09-434-122-33	Sequence 33, Appli
40	409	60.7	106	3	US-08-397-411-9	Sequence 9, Appli
41	409	60.7	599	1	US-08-463-163-3	Sequence 3, Appli
42	408	60.5	100	2	US-08-308-494A-19	Sequence 19, Appli
43	408	60.5	106	1	US-07-634-278-1	Sequence 1, Appli
44	408	60.5	106	1	US-07-634-278-16	Sequence 16, Appli
45	408	60.5	106	1	US-08-477-728-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-171-945-17
; Sequence 17, Application US/09171945
; Patent No. 6277599

; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen

; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek

; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29

; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14

; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04

; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29

; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-17

Alignment Scores:

Pred. No.: 8.33e-47
Score: 458.00
Percent Similarity: 83.76%
Best Local Similarity: 76.92%
Query Match: 67.95%
DB: 3
Length: 235
Matches: 90
Conservative: 8
Mismatch: 19
Indels: 0
Gaps: 0

US-10-049-868A-1 (1-359) x US-09-171-945-17 (1-235)

QY 1 GACATTGAGTCCACCAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGTCCACC 60
Db 23 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 42
QY 61 ATGACCTGAGTCCAGTCTCAAGTGTAAATTACATGCACTGGTTCACAGCAGAGTCGGGC 120
Db 43 IleThrCysSerAlaSerSerValThrTyrMetHisTrpPheGlnLysProGly 62
QY 121 ACCTTCCCAAGAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTCTCGC 180
Db 63 ThrSerProLysLeuTrpIleThrSerAsnLeuAlaSerGlyValProAlaArg 82
QY 181 CTCAGTGCAGTGGTCTGGGACAGAAATCCACCTGGAAATCAGTAGAGTGAAGCTGAG 240
Db 83 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 102
QY 241 CATGTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCAGGTTGGTCTGGG 300
Db 103 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 122
QY 301 ACCAAGCTGGAGTGAAGGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 123 ThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhe 139
RESULT 2
5455030-3
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 3
; LENGTH: 215
5455030-3
Alignment Scores:
Pred. No.: 3,01e-45 Length: 215
Score: 445.00 Matches: 90
Percent Similarity: 82.76% Conservative: 6
Best Local Similarity: 77.59% Mismatches: 18
Query Match: 66.02% Indels: 2
DB: 6 Gaps: 1
US-10-049-868A-1 (1-359) x 5455030-3 (1-215)
QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGTCCACATGACCTGC 69
Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23
QY 70 AGTGCAGTTCAGTGT-----AATTACATGCACTGGTTCAGCGAGAGTGGGCACC 123
Db 24 ArgAlaSerSerValSerSerTyrLeuHisTrpPheGlnLysSerGlyAla 43
QY 124 TTCCCAAGAGAGGATTTATGACATCCAACTGGCTTCTGGAGTCCCTGTCTGGCTC 183
Db 44 SerProLysLeuTrpIleThrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63
QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTCGAATCATGAGTGAAGGCTGAGGAT 243

Db 64 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83
QY 244 GTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTTCTGGGACC 303
Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103
QY 304 AAGCTGGAGCTGAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 104 LysLeuGluLeuLysArgAlaAspAlaProIleValSerIlePhe 119
RESULT 3
US-08-303-569B-5
; Sequence 5, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Achwal, Diljeet S.
; APPLICANT: Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-303-569B-5
Alignment Scores:
Pred. No.: 3,11e-45 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 2 Gaps: 0
US-10-049-868A-1 (1-359) x US-08-303-569B-5 (1-235)
QY 4 ATTGAGTCCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGTCCACATG 63
Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGAGTCCAGTTCAGTGTAAATTACATGCACTGGTTCACAGCAGAGTGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCAAGAGAGGATTTATGACATCCAACTGGCTTCTGGAGTCCCTGTCTGGCTC 183
Db 64 SerProLysArgTrpIleThrSerThrSerLysLeuAlaSerGlyValProAlaHisPhe 83

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGGTCCACCATG 63
Db |||||
24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCAGTTCAGTGTAAATACATGCACCTGGTTCACGACGAGGTCCGGGCACC 123
Db |||||
44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCAAGAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTCTCGCCTC 183
Db |||||
64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGCAGTGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGCTCAGGAT 243
Db |||||
84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTAATCTGTCACCAACTGTAGAGTATCCGCTCACCTTCGGTCTGGGACC 303
Db |||||
104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db |||||
124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 6

US-09-348-224-5
; Sequence 5, Application US/09348224

; Patent No. 6750325

; GENERAL INFORMATION:

; APPLICANT: Jolliffe, Linda Kay

; APPLICANT: Zivin, Robert Allan

; APPLICANT: Adair, John Robert

; APPLICANT: Athwal, Diljeet Singh

; TITLE OF INVENTION: CD3 Specific Recombinant Antibody

; FILE REFERENCE: CARP0066

; CURRENT APPLICATION NUMBER: US/09/348,224

; EARLIER FILING DATE: 1999-07-06

; EARLIER APPLICATION NUMBER: 08/116,247

; EARLIER FILING DATE: 1993-09-03

; EARLIER APPLICATION NUMBER: 07/743,377

; EARLIER FILING DATE: 1991-10-04

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Mouse

US-09-348-224-5

Alignment Scores:
Pred. No.: 3,11e-45 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-348-224-5 (1-235)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGGTCCACCATG 63
Db |||||
24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCAGTTCAGTGTAAATACATGCACCTGGTTCACGACGAGGTCCGGGCACC 123
Db |||||
44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCAAGAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTCTCGCCTC 183
Db |||||
64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGTTCAGGAT 243
Db |||||

Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTAATCTGTCACCAACTTGTAGAGTATCCGCTCACCTTCGGTCTGGGACC 303
Db |||||
104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db |||||
124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 7

US-09-553-498-8

; Sequence 8, Application US/09553498

; Patent No. 6309861

; GENERAL INFORMATION:

; APPLICANT: Ambrosius, Dorothee

; APPLICANT: Rudolph, Rainer

; APPLICANT: Schaeffner, Joerg

; APPLICANT: Schwarz, Elisabeth

; TITLE OF INVENTION: Process for the production of naturally folded and secreted prot

; FILE REFERENCE: Case 20379

; CURRENT APPLICATION NUMBER: US/09/553,498

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: EP99107412.1

; PRIOR FILING DATE: 1999-04-26

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 8

; LENGTH: 255

; TYPE: PRT

; ORGANISM: E. coli

US-09-553-498-8

Alignment Scores:
Pred. No.: 4,24e-45 Length: 255
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-553-498-8 (1-255)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGGTCCACC 60
Db |||||
132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151
QY 61 ATGACCTGCAGTCCCGAGTTCAGTGTAAATACATGCACCTGGTTCACGACGAGGTCCGGC 120
Db |||||
152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly 171
QY 121 ACCTTCCCAAGAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTCTCGC 180
Db |||||
172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGTGAG 240
Db |||||
192 PheSerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 211
QY 241 GATGTGGTGTGTAATCTGTCACCAACTGTAGATATCCGCTCAGTTCCGTTCCGTTGGG 300
Db |||||
212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db |||||
232 ThrLysLeuGluLeuLysArgAlaAla 241

RESULT 8

US-09-618-869-8

; Sequence 8, Application US/09618869

; Patent No. 6455279

; GENERAL INFORMATION:

; APPLICANT: Ambrosius, Dorothee

; APPLICANT: Rudolph, Rainer

```

; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-8

Alignment Scores:
Pred. No.: 4,246-45 Length: 255
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-618-869-8 (1-255)

Qy 1 GACATTGAGTCACCCAGTCTCCAGCATCATGTCATCTCCAGGGGAGAGGTCAACC 60
Db 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151
Qy 61 ATGACCTGCGAGTCCAGTTCAGTGTAAATACATGCACTGGTCCACGAGGTCCGGC 120
Db 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly 171
Qy 121 ACCTTCCCAAGAGAGATTATGACACATCCAACTGGCTTCGGAGTCCCTCGCTCGC 180
Db 172 ThrSerProLysArgTyrIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191
Qy 181 CTCAGTGGCAGTGGTCTGGGACAGAAATCCCTCGGAATCAGTAGTGAAGCTGAG 240
Db 192 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 211
Qy 241 GATGTGGGTGTATTACTGTCAACAACCTTGAGTATCCGTCACGTCCTGGGTGGGG 300
Db 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231
Qy 301 ACCAAGCTGGAGCTGAACGGGCTGATGCT 330
Db 232 ThrLysLeuGluLeuLysArgAlaAlaAla 241

RESULT 9
US-08-737-129A-4
; Sequence 4, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: NO. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-4

Alignment Scores:
Pred. No.: 4,56e-45 Length: 213
Score: 443.50 Matches: 86
Percent Similarity: 83.76% Conservative: 12
Best Local Similarity: 73.50% Mismatches: 18
Query Match: 65.80% Indels: 1
DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x US-08-737-129A-4 (1-213)

Qy 1 GACATTGAGTCACCCAGTCTCCAGCATCATGTCATCTCCAGGGGAGAGGTCAACC 60
Db 1 GluLeuValMetThrGlnThrProAlaIleMetSerAlaSerProGlyGluLysValThr 20
Qy 61 ATGACCTGCGAGTCCAGTTCAGTGTAAATACATGCACTGGTCCACGAGGTCCGGC 120
Db 21 MetThrCysSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGly 40
Qy 121 ACCTTCCCAAGAGAGATTATGACACATCCAACTGGCTTCGGAGTCCCTCGCTCGC 180
Db 41 ThrProLysArgTyrIleTyrGlyThrSerLysLeuThrSerGlyValProAlaArg 60
Qy 181 CTCAGTGGCAGTGGTCTGGGACAGAAATCCACCTCGAAATCAGTAGAGTGAAGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerPheSerLeuThrIleSerSerMetGluAlaGlu 80
Qy 241 GATGTGGGTGTATTACTGTCAACAACCTTGAGTATCCGTCACGTCCTGGGTGGGG 300
Db 81 AspAlaAlaThrTyrTyrCysHisGlnArgSerSerTyrPro---ThrPheGlyGlyGly 99
Qy 301 ACCAAGCTGGAGCTGAACGGGCTGATGCTGCCAACCTGTATCCATCTTC 351
Db 100 ThrLysLeuGluLeuLysArgAlaAspAlaAlaproThrValSerIlePhe 116

RESULT 10
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14

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;; PRIOR APPLICATION NUMBER: GB9609405.7

;; PRIOR FILING DATE: 1996-05-04

;; PRIOR APPLICATION NUMBER: PCT/GB97/01165

;; PRIOR FILING DATE: 1997-04-29

;; NUMBER OF SEQ ID NOS: 131

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 9

;; LENGTH: 108

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-9

Alignment Scores:
Pred. No.: 1,25e-44 Length: 108
Score: 439.00 Matches: 86
Percent Similarity: 85.13% Conservative: 6
Best Local Similarity: 79.63% Mismatches: 16
Query Match: 65.13% Indels: 0
DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-171-945-9 (1-108)

QY 1 GACATTGAGCTCACCCAGCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCAAC 60
DB 1 AspileGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACTGAGTGCAGTTCAGTGTAAATTACATGCATCTGTTCCAGCAGGAGTCGGGC 120
DB 21 IleThrCysSerAlaSerSerValThrTyrMetHisTrpPheGlnGlnLysProGly 40
QY 121 ACCTTCCCAAAAGAGGATTTATGACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
DB 41 ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATCACCTGGAAATCAGTAGAGTGAAGGTGAG 240
DB 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 80
QY 241 GATGTGGGTGTATTACTGTCAACACTTGTAGAGTATCCGCTCAGTTCGGTGTGGG 300
DB 81 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 100
QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
DB 101 ThrLysLeuGlnLeuLysArgAla 108

RESULT 11

US-09-526-738A-2

;; Sequence 2, Application US/09526738A

;; Patent No. 6630584

;; GENERAL INFORMATION:

;; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT

;; APPLICANT: LTD.

;; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53

;; FILE REFERENCE: 1196336

;; CURRENT APPLICATION NUMBER: US/09/526, 738A

;; CURRENT FILING DATE: 2000-03-16

;; NUMBER OF SEQ ID NOS: 9

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 2

;; LENGTH: 256

;; TYPE: PRT

;; ORGANISM: Humanus

US-09-526-738A-2

Alignment Scores:
Pred. No.: 4.83e-43 Length: 256
Score: 427.00 Matches: 84
Percent Similarity: 80.70% Conservative: 8
Best Local Similarity: 73.68% Mismatches: 22
Query Match: 63.35% Indels: 0

DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-526-738A-2 (1-256)

QY 1 GACATTGAGCTCACCCAGCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCAAC 60
DB 132 AspileGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151
QY 61 ATGACTGAGTGCAGTTCAGTGTAAATTACATGCATCTGTTCCAGCAGGAGTCGGGC 120
DB 152 IleThrCysSerAlaSerSerValAsnTyrMetHisTrpPheGlnGlnLysProGly 171
QY 121 ACCTTCCCAAAAGAGGATTTATGACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
DB 172 ThrSerProLysLeuTrpIleSerThrSerAsnLeuAlaSerGlyValProAlaArg 191
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATCACCTGGAAATCAGTAGAGTGAAGGTGAG 240
DB 192 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 211
QY 241 GATGTGGGTGTATTACTGTCAACACTTGTAGAGTATCCGCTCAGTTCGGTGTGGG 300
DB 212 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProTyrThrPheGlyGlyGly 231
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCACTGTA 342
DB 232 ThrLysLeuGlnIleLysArgAlaAlaGlyAlaProVal 245

RESULT 12

US-09-526-738A-4

;; Sequence 4, Application US/09526738A

;; Patent No. 6630584

;; GENERAL INFORMATION:

;; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT

;; APPLICANT: LTD.

;; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53

;; FILE REFERENCE: 1196336

;; CURRENT APPLICATION NUMBER: US/09/526, 738A

;; CURRENT FILING DATE: 2000-03-16

;; NUMBER OF SEQ ID NOS: 9

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 4

;; LENGTH: 258

;; TYPE: PRT

;; ORGANISM: Humanus

US-09-526-738A-4

Alignment Scores:
Pred. No.: 4.84e-43 Length: 258
Score: 427.00 Matches: 84
Percent Similarity: 80.70% Conservative: 8
Best Local Similarity: 73.68% Mismatches: 22
Query Match: 63.35% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-526-738A-4 (1-258)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCAAC 60
DB 134 AspileGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 153
QY 61 ATGACTGAGTGCAGTTCAGTGTAAATTACATGCATCTGTTCCAGCAGGAGTCGGGC 120
DB 154 IleThrCysSerAlaSerSerValAsnTyrMetHisTrpPheGlnGlnLysProGly 173
QY 121 ACCTTCCCAAAAGAGGATTTATGACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
DB 174 ThrSerProLysLeuTrpIleSerThrSerAsnLeuAlaSerGlyValProAlaArg 193
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATCACCTGGAAATCAGTAGAGTGAAGGTGAG 240
DB 194 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 213

